







|          |   |    |  |
|----------|---|----|--|
| DR       | EMBL; BC016381; AAH16381.1; -.  | RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Mizny D.M., Soderberg E.J., Lu X., Gibbs R.A., InterPro; IPR003599; IG_1-like.  |
| DR       | InterPro; IPR007110; IG_1-like.   | RA | Pahey J., Heiton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., InterPro; IPR003597; IG_c1.  |
| DR       | InterPro; IPR003006; IG_MHC.  | RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krywinski M.I., Smailus D.E., Schnarch A., Schein J.E., InterPro; IPR00596; IG_3.  |
| DR       | SMART; SM00409; C1-set; 3.  | RA | Jones S.J., Marra M.A., SMART; SM00409; IG_2.  |
| DR       | SMART; SM00407; IGC1; 3.  | RA | SMART; SM00406; IGV; 1.  |
| DR       | PROSITE; PS50035; IG_LIKE; 4.   | RA | PROSITE; PS00290; IG_MHC; UNKNOWN_2.   |
| DR       | PROSITE; PS00290; IG_MHC; UNKNOWN_2.  | RA | KW Hypothetical protein.   |
| SEQUENCE | 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;   | RP | SEQUENCE FROM N.A.   |
| SEQUENCE | 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;   | RC | SEQUENCE=Spine;  |
| Query    | Query Match 42.8%; Best Local Similarity 65.3%; Matches 243; Conservative 15; Mismatches 47; Indels 67; Gaps 7; | RA | Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  |
| Db       | 223 WLNCEBILYPRMLQDNAAENVY---VWKOYVVDV-----KAVTSNIV 259   | DR | EMBL; BC073782; AAH73782.1; -.   |
| Db       | 113 YYCARDLALWLSGFTDKEKYGLDVGQTPVSSASTKGPVFLPAPSSKTSGGT 172   | DR | InterPro; IPR003599; IG_1-like.  |
| Db       | 260 ASVQCDNSDKFP-----VYKYPGKGCPTIGDEG-----DT 289  | DR | InterPro; IPR007110; IG_1-like.  |
| Db       | 173 AALGCVYDQDFPEPYTVSSNNSGALTSGVTFPAA----VQSSGLYLSVSVTPSSSLGT 228  | DR | InterPro; IPR003597; IG_1-like.  |
| Db       | 290 DLY----DYYPEEDIEGDKYRP-----HTCOPCPDAPEALGAPSFLPPPKPDKTLMISR 339   | DR | InterPro; IPR003596; IG_1-like.  |
| Db       | 229 QTYICVNHNKPSNTKVDKRVPEPKSCDKTHTCOPCPAPELLGGPSVFLPPKPKPDKTLMISR 288  | DR | InterPro; IPR003596; IG_1-like.  |
| Db       | 340 TPEVTCVVVDVSHEDPEVKENWYDGVENVAKTKPREEQNSTYRVVSVLTVLHQDWLWN 399  | DR | InterPro; IPR003596; IG_1-like.  |
| Db       | 289 TPEVTCVVVDVSHEDPEVKENWYDGVENVAKTKPREEQNSTYRVVSVLTVLHQDWLWN 348  | DR | InterPro; IPR003596; IG_1-like.  |
| Db       | 400 GKEYKCKVSNKALPVPIEKTKISAKGQPREQVYTLPPSREEMTKNQVSLTCLYKGFYPS 459   | DR | InterPro; IPR003596; IG_1-like.  |
| Db       | 349 GKEYKCKVSNKALPAEKTKISAKGQPREQVYTLPPSREEMTKNQVSLTCLYKGFYPS 408   | DR | InterPro; IPR003596; IG_1-like.  |
| Db       | 460 DIAVEMENGOPENNYKTPVLDSDGSFFLYSKETVDKSRWQGQNVFSCSVMEHALNH 519  | DR | InterPro; IPR003596; IG_1-like.  |
| Db       | 409 DIAVEMENGQOPENNYKTPVLDSDGSFFLYSKLTVDKSRWQGQNVFSCSVMEHALNH 468   | DR | InterPro; IPR003596; IG_1-like.  |
| Db       | 520 YTQKSLSLSPGK 531  | DR | InterPro; IPR003596; IG_1-like.  |
| Db       | 469 YTQKSLSLSPGK 480  | DR | InterPro; IPR003596; IG_1-like.  |
| RESULT 4 | Q6GMW7 PRELIMINARY: PRT; 475 AA.  | Db | EDDTGDKVRP-----HTCPPCPAPEALGAPSFLFPKPKDTLMISRPEVTCVVVD 350   |
| ID       | Q6GMW7 PRELIMINARY: PRT; 475 AA.  | Db | SNTKDVKVKVPKSKTKHTPPCPPELIGPSVLFPPKPKDTLMISRPEVTCVVVD 294  |
| AC       | Q6GMW7; PMID:22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;   | Qy | 351 SHEDDEVKENWYDGVENVAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 410  |
| DT       | 05-JUL-2004 (TREMBLrel. 27, Created)  | Db | 295 SHEDDEVKENWYDGVENVAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 354  |
| DT       | 05-JUL-2004 (TREMBLrel. 27, Last sequence update)   | Qy | 411 ALPVPTEKTIKSKARGQPREQVYTLPPSREEMTKNQVSLTCLYKGFYPSDIAVEMENGQ 470  |
| DT       | 05-JUL-2004 (TREMBLrel. 27, Last annotation update)   | Db | 355 ALPAPTEKTIKSKARGQPREQVYTLPPSREEMTKNQVSLTCLYKGFYPSDIAVEMENGQ 414  |
| DE       | Hypothetical Protein.   | Qy | 471 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGQNVFSCSVMEHALNHYTQKSLSLSPG 530  |
| OS       | Homo sapiens (Human)  | Db | 415 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGQNVFSCSVMEHALNHYTQKSLSLSPG 474  |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   | Qy | 531 K 531  |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  | Db | 475 K 475  |
| OX       | NCBI_TaxID=9606;  | Qy | RESULT 5   |
| RN       | [1]   | Db | Q6PJA4 PRELIMINARY; PRT; 470 AA.   |
| RP       | SEQUENCE FROM N.A.  | RC | SEQUENCE=Spine;  |
| RX       | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  | RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner C.M., Schenck A., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruska A., Farmer A., Rubin G.M., Hong L., Stoeckert M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahy S.J., |

|          |  |                    |  |     |
|----------|--|--------------------|--|-----|
| AC       | Q6PJA4;  | 383                | TYRVSILTVLHQDWLKGKYCKVSKNPKVPLKTIKAKGQPREPOVYTLPPSREEM | 442 |
| DT       | 05-JUL-2004 (TREMBrel. 27, Created)  |                    |  |     |
| DT       | 05-JUL-2004 (TREMBrel. 27, Last sequence update)                             |                    |  |     |
| DT       | 05-JUL-2004 (TREMBrel. 27, Last annotation update)                           |                    |  |     |
| DE       | Hypothetical protein.  |                    |  |     |
| OS       | Homo sapiens (Human).  |                    |  |     |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;            |                    |  |     |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                   |                    |  |     |
| OX       | NCBI_TaxID=9606;   |                    |  |     |
| RN       | SEQUENCE FROM N.A.   |                    |  |     |
| RC       | TISSUE=Primary B-Cells;  |                    |  |     |
| RA       | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;               |                    |  |     |
| RA       | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,                     |                    |  |     |
| RA       | Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schulter G.D.,          |                    |  |     |
| RA       | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,            |                    |  |     |
| RA       | Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,              |                    |  |     |
| RA       | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,                |                    |  |     |
| RA       | Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,        |                    |  |     |
| RA       | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,           |                    |  |     |
| RA       | Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,         |                    |  |     |
| RA       | Bosak S.A., McEvany P.J., McKerian K.J., Malek J.A., Gunaratne P.H.,         |                    |  |     |
| RA       | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,        |                    |  |     |
| RA       | Villalon D.K., Muzny D.M., Soderberg E.J., Iu X., Gibbs R.A.,                |                    |  |     |
| RA       | Fahey J., Helton E., Kettenman M., Madan A., Rodrigues S., Sanchez A.,       |                    |  |     |
| RA       | Whiting M., Madan A., Young J.W., Shvchenko Y., Bouffard G.G.,               |                    |  |     |
| RA       | Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,                     |                    |  |     |
| RA       | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,       |                    |  |     |
| RA       | Jones S.J., Marra M.A., Skalska U., Smialus D.E., Schenrich A., Schein J.E., |                    |  |     |
| RA       | RT   | SEQUENCE FROM N.A. |  |     |
| RC       | TISSUE=Primary B-Cells;  |                    |  |     |
| RA       | Strausberg R.;   |                    |  |     |
| RA       | Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.                     |                    |  |     |
| RL       | EMBL: BC018747; AAH18747.1;  |                    |  |     |
| DR       | HSSP: P01861; IADQ.  |                    |  |     |
| DR       | InterPro: IPR001599; Ig-like.  |                    |  |     |
| DR       | InterPro: IPR007110; Ig-cl.  |                    |  |     |
| DR       | InterPro: IPR001597; Ig-cl.  |                    |  |     |
| DR       | InterPro: IPR003006; Ig-MHC.   |                    |  |     |
| DR       | InterPro: IPR003596; Ig-v.   |                    |  |     |
| PFAM     | PF07654; Cl-beta; 3.   |                    |  |     |
| DR       | SMART: SMART00409; Ig; 2.  |                    |  |     |
| DR       | SMART: SMART00409; Ig; 1.  |                    |  |     |
| DR       | SMART; SMART00406; IgV; 1.   |                    |  |     |
| DR       | PROSITE; PS50835; Ig-LIKE; 4.  |                    |  |     |
| DR       | PROSITE; PS50290; Ig-MHC; UNKNOWN_2.   |                    |  |     |
| KW       | Hypothetical Protein.  |                    |  |     |
| SEQUENCE | 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;                                    |                    |  |     |
| SQ       | Query Match 42.7%; Score 1211; DB 2; Length 470;                             |                    |  |     |
|          | Best Local Similarity 63.8%; Pred. No. 5.1e-75;                              |                    |  |     |
| Matches  | 248; Conservative 18; Mismatches 61; Indels 62; Gaps 8;                      |                    |  |     |
| Qy       | 191 DTLLQENSLTYIPKGFGPSHLLPFAPLHGNPMLCNCPBILYFPRMLDDNAENY-----               | 243                |  |     |
| Db       | 96 NSLYLQWNSLRAEDTAYD----WFDWGGTLYTSSASTKG 145                               |                    |  |     |
| Qy       | 244 -YWKQVVDKAVTSNVAQVCDNSDKP-----VYKYPKGCGPTLGDEG 287                       |                    |  |     |
| Db       | 146 PSVPLAPSSKTSGGTAAALGCLVYDPEPVTVWSNSGALISGVHTPEA----VLQSSG 201            |                    |  |     |
| Qy       | 288 -----DTDLY----DYPBPEDTEGDKVRP-----HTCPCPAPEALCAP 322                     |                    |  |     |
| Db       | 202 LYSSLSSVVTVPSSSLGRTYICVNHKPSNTKVDKCKEPKSDKTHTCPPCPAPELIGGP 261           |                    |  |     |
| Qy       | 323 SYLFPPKPKDTMISPTPENTCYVVDVPSHEDEPVKENVYDGEVVKAKTPREEQYNS 382             |                    |  |     |
| Db       | 262 SYLFPPKPKDTMISPTPENTCYVVDVPSHEDEPVKENVYDGEVVKAKTPREEQYNS 321             |                    |  |     |



RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Dickson M.C.,' Green E.D., Schmitz J., Myers R.M., Butterfield Y.S.,' RA Rodriguez A.C., Grimwood J., Smailus D.E., Schnierch A., Schein J.E.,' RA Krzywinski M.I., Skalska U., Smailus D.E., Schnierch A., Schein J.E.,' RA Jones S.J., Marra M.A./ "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [2]

SEQUENCE FROM N.A.

RP TISSUE= spleen;

RA Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RL EMBL; BX640620; CAB45774.1; -.

DR HSSP; P01861; IADQ.

DR InterPro; IPR03599; I9.

DR InterPro; IPR03599; I9.

DR InterPro; IPR027110; I9-like.

DR InterPro; IPR03597; I9-cl.

DR InterPro; IPR03006; I9-MHC.

DR InterPro; IPR03596; I9-v.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IGC1; 3.

DR SMART; SM00407; IGC1; 1.

DR PROSITE; PS0835; I9-LIKE; 4.

DR PROSITE; PS00290; I9-MHC; UNKNOWN\_2.

DR Hypothetical protein.

SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match 42.6%; Score 1210; DB 2; Length 476;

Best Local Similarity 62.6%; Pred. No. 6.4e-75;

Matches 244; Conservative 20; Mismatches 53; Indels 73; Gaps 7;

Db 190 IDTLLQENSLTYTIPKOFFGSHLPLPWNLCNEILYFRRWYQDNEAENV-----

Db 102 LSLLRABDTAVYCARFCFGN-----

Qy 190 IYKYPGKGCPYLGE-----

Db 141 GRSVFLAPSSSSTSGTAALGCLVXDFPPVTVSNNSGALTSGVHTEFPA---VQLOSS 196

Qy 244 --YWKQVVDVKAVTENVASYQCDNSDKFP-----

Db 141 GRSVFLAPSSSSTSGTAALGCLVXDFPPVTVSNNSGALTSGVHTEFPA---VQLOSS 196

Qy 287 G-----DIDLY----DYPVBEDETEGDKVRP-----

Db 197 GLYSLSVVTVTPSSSLGQTQYICNVNWKPSNTKVDDKVEPKSCDKTHTCPCPAPELIGG 256

Qy 322 PSVFLFPKPKDITLMISRTPETVCTVYVDVSHEDPEVFKNWTGVEVHNAKTKPREEQYN 381

Db 257 PSVFLFPKPKDITLMISRTPETVCTVYVDVSHEDPEVFKNWTGVEVHNAKTKPREEQYN 316

Qy 382 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPVPIEKTKSAGQPREPQVYTLPPSREE 441

Db 317 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPVPIEKTKSAGQPREPQVYTLPPSREDE 376

Qy 442 MTKNQVSILTCLVKGFYPSDIAVEWENGOPENNYKTPPVLDGSFLYSKLTVDKSRW 501

Db 377 LTKNQVSILTCLVKGFYPSDIAVEWENGOPENNYKTPPVLDGSFLYSKLTVDKSRW 436

RESULT 10

Q6P181 PRELIMINARY; PRT; 478 AA.

AC Q6P181; PRELIMINARY; PRT; 478 AA.

DB Hypothetical protein DKFZp686I15196.

GN Name=DKFZp686I15196;

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1] \_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Primary\_B-Cell; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wang J., Heieh F.,



Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY570731; ASN88328.1; -.  
 DR HSSP; P01857; 1A07.  
 GO; GO:004872; F; receptor activity; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003587; Ig-cl.  
 DR InterPro; IPR003066; Ig\_MHC.  
 DR Pfam; PRO7654; C1\_set; 3.  
 SMART; SM00407; IgCl; 3.  
 PROSITE; PS50835; Ig\_LIKE; 3.  
 PROSITE; PS00290; Ig\_MHC; UNKNOWN\_2.  
 Receptor.  
 KW NON\_TER 1 38162 MW; DD96C3D7E0BE5845 CRC64;  
 SEQUENCE 348 AA; 1 38162 MW; DD96C3D7E0BE5845 CRC64;  
 Query Match 42.6%; Score 1208; DB 2; Length 348;  
 Best Local Similarity 74.0%; Pred. No. 5.6e-75; Indels 44; Gaps 5;  
 Matches 236; Conservative 9; Mismatches 30; DR SMART; SM00020; Tryp\_SPC; 1.  
 DR SMART; SM00022; EGF\_1; UNKNOWN\_1.  
 DR SMART; SM000407; IgCl; 1.  
 DR SMART; SM00069; Gla; 1.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00190; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS00186; EGF\_2; 1.  
 DR PROSITE; PS00026; EGF\_3; 1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; Gla\_1; 1.  
 DR PROSITE; PS00335; Ig\_LIKE; 2.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW EGF-like domain; Hydrolase; Protease; Serine protease.  
 SEQUENCE 679 AA; 0B0023AE70A067A1 CRC64;  
 Query Match 42.6%; Score 1208; DB 2; Length 679;  
 Best Local Similarity 82.4%; Pred. No. 1.3e-74; Indels 26; Gaps 2;  
 Matches 230; Conservative 4; Mismatches 19; DR 277 GKCPTLGDEGTDLYDYPE-----  
 DR 403 GQCCATVGHFGVYTRVSQYIEWLQKLNRSRPEPQGVLLRAPPFQSAEPKSCDKT-----HTCPP 460  
 DR 313 CPAPEALGAPSVLFLPPKPKDTLMSRPEVTCVVDVYSHDEPEVKENWYDGVEVNAK 372  
 DR 461 CRRAPLGGSVFLPPKPKDTLMSRPEVTCVVDVYSHDEPEVKENWYDGVEVNAK 520  
 DR 373 TKPREEQNSTYRVSVLTVHQDWLNGKEYCKVSNKALPVPIEKTKSIAKGQPREQV 432  
 DR 521 TKPREEQNSTYRVSVLTVHQDWLNGKEYCKVSNKALPAEKTKSIAKGQPREQV 580  
 DR 433 YTLPPSREEMTKNOVSLTCLVKGRPSDIAVEMESQPNYYKTPVLDSDGSFFLYS 492  
 DR 581 YTLPPSREDELTKNOVSLTCLVKGRPSDIAVEMESQPNYYKTPVLDSDGSFFLYS 640  
 DR Hypothetical protein.  
 DR Homo\_sapiens (Human).  
 DR Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 DR NCBITaxID=9606; -.  
 DR SEQUENCE FROM N.A.  
 DR MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;  
 DR Hu Z.; Garen A.;  
 DR "Targeting tissue factor on tumor vascular endothelial cells and tumor  
 cells for immunotherapy in mouse models of prostatic cancer.";  
 DR Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
 DR Factor VII active site mutant immunoconjugate.  
 DR Homo\_sapiens (Human).  
 DR Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.  
 DR Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 DR NCBITaxID=9606; -.  
 DR GO:0005576; C\_extracellular; IEA.  
 DR GO:0005509; C calcium ion binding; IEA.  
 DR GO:0008233; F\_peptidase activity; IEA.  
 DR GO:0004295; F\_trypsin activity; IEA.  
 RN RESULT 13  
 O96PQ8 PRELIMINARY; PRT; 679 AA.  
 ID Q96PQ8; PRELIMINARY; PRT; 679 AA.  
 AC Q96PQ8; PRELIMINARY; PRT; 679 AA.  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DR Factor VII active site mutant immunoconjugate.  
 OS Homo\_sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBITaxID=9606; -.  
 RN RP SEQUENCE FROM N.A.  
 RN MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;  
 RN Hu Z.; Garen A.;  
 RN "Targeting tissue factor on tumor vascular endothelial cells and tumor  
 cells for immunotherapy in mouse models of prostatic cancer.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
 RN SEQUENCE FROM N.A.  
 RN Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RN EMBL; AY570731; ASN88328.1.  
 DR GO:0005576; C\_extracellular; IEA.  
 DR GO:0005509; C calcium ion binding; IEA.  
 DR GO:0008233; F\_peptidase activity; IEA.  
 DR GO:0004295; F\_trypsin activity; IEA.  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;

BESUIT 1

|  |  |             |        |            |                    |    |  |
|--|--|-------------|--------|------------|--------------------|----|--|
| Copyright (c) 1993 - 2005 Compugen Ltd.  | GenCore version 5.1.6                          | 26          | 1357.5 | 47.8       | 640                | 8  | ADP76035   |
| OM protein - protein search, using sw model  |  | 27          | 1324   | 46.6       | 629                | 8  | ADP76037   |
| Run on: May 24, 2005, 05:54:10 ; Search time 162 Seconds (without alignments)  | 1267.715 Million cell updates/sec              | 28          | 1279   | 45.1       | 800                | 7  | Ade03635   |
| Title: US-10-068-426-5   | 2839   | 29          | 1237   | 43.6       | 313                | 2  | AAW53321   |
| Perfect score: 1   | MPLLLLLLPSPLHHPIC.....MHEALHHHTYQKSLSLSPQK 531 | 30          | 1237   | 43.6       | 313                | 2  | AY29766  |
| Sequence:  |  | 31          | 1237   | 43.6       | 313                | 5  | AGG77946   |
| Scoring table: BLOSUM62  | Gapext 10.0 , Gapext 0.5                       | 32          | 1237   | 43.6       | 313                | 6  | Abr39961   |
| Searched: 2105692 seqs, 386760381 residues   |  | 33          | 1235.5 | 43.5       | 420                | 5  | Aae15348   |
| Total number of hits satisfying chosen parameters: 2105692   |  | 34          | 1234   | 43.5       | 778                | 2  | Aaw15489   |
| Minimum DB seq length: 0   |  | 35          | 1222.5 | 43.4       | 470                | 6  | Abr61415   |
| Maximum DB seq length: 20000000000   |  | 36          | 1231   | 43.4       | 581                | 8  | ADP03590   |
| Post-processing: Minimum Match 0% Maximum Match 100%   | Listing first 45 summaries                     | 37          | 120.5  | 43.3       | 401                | 2  | Aaw10537   |
| Database : A_Geneseq_16Dec04:*   |  | 38          | 1230   | 43.3       | 388                | 8  | AAAMS0248  |
| 1: geneseqP1980s:*   |  | 39          | 1230   | 43.3       | 388                | 8  | ADQ76791   |
| 2: geneseqP1990s:*   |  | 40          | 1230   | 43.3       | 449                | 2  | Aaw96278   |
| 3: geneseqP2000s:*   |  | 41          | 1230   | 43.3       | 502                | 6  | ABJ37109   |
| 4: geneseqP2001s:*   |  | 42          | 1230   | 43.3       | 502                | 8  | ADQ79922   |
| 5: geneseqP2002s:*   |  | 43          | 1230   | 43.3       | 542                | 5  | Aau76357   |
| 6: geneseqP2003s:*   |  | 44          | 1228.5 | 43.3       | 528                | 5  | Aau79654   |
| 7: geneseqP2004s:*   |  | 45          | 1228.5 | 43.3       | 528                | 8  | ADN59105   |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. |  |             |        |            |                    |    |  |
| SUMMARIES  |  |             |        |            |                    |    |  |
| Result No.   | Score  | Query Match | Length | DB ID      | Description        |    |  |
| 1  | 233.9  | 100.0       | 531    | 5 ABB78238 | Abb78238 Amino aci | XX | WO200263003-A2.  |
| 2  | 2829   | 99.6        | 531    | 5 ABB78237 | Abb78237 Amino aci | XX | 15-AUG-2002.   |
| 3  | 2822.5   | 99.4        | 544    | 5 ABB78236 | Abb78236 Amino aci | XX |  |
| 4  | 2812.5   | 99.4        | 531    | 5 ABB78239 | Abb78239 Amino aci | XX | 06-FEB-2002; 2002WO-US003549.  |
| 5  | 2812.5   | 99.1        | 544    | 5 ABB78234 | Abb78234 Amino aci | XX | 06-FEB-2001; 2001US-0266838P.  |
| 6  | 2812.5   | 99.1        | 544    | 5 ABB78235 | Abb78235 Amino aci | PR |  |
| 7  | 2411.5   | 84.9        | 562    | 3 AAY49933 | Aay49933 Human gly | XX | (GEMY ) GENETICS INST LLC.   |
| 8  | 2381.5   | 83.9        | 568    | 3 AAY49935 | Aay49935 Human gly | PA |  |
| 9  | 1615.5   | 56.9        | 626    | 4 AAE12135 | Aae12135 Human gly | XX |  |
| 10   | 1610.5   | 56.9        | 626    | 7 ADF63094 | Adf63094 Human MBP | PI | Shaw GB, Kumar R, Sako DS, McDonagh T, Sullivan FX,  |
| 11   | 1615.5   | 56.9        | 626    | 7 ADJ58624 | Adj58624 Human hea | XX | WPI ; 2002-657537/70.  |
| 12   | 1615.5   | 56.9        | 626    | 8 ADH40324 | Adh40324 Human pla | DR | DR N-PSDB; ABQ78665.   |
| 13   | 1615.5   | 56.9        | 626    | 8 ADQ59833 | Adq59833 Human myo | XX |  |
| 14   | 1516   | 54.1        | 290    | 5 ABB78244 | Abb78244 Amino aci | PT | New glycoprotein Ib alpha fusion polypeptides, useful for treating a disorder associated with platelet activation e.g. ischaemic heart disease, stroke, venous or arterial thrombosis or atherosclerosis.                          |
| 15   | 1527   | 53.8        | 301    | 5 ABB78240 | Abb78240 Amino aci | PT | The present sequence represents a fusion protein of glycoprotein 1B-alpha (GP1B) and an immunoglobulin (Ig) polypeptide. The fusion protein  |
| 16   | 1526   | 53.8        | 290    | 5 ABB7243  | Abb7243 Amino aci  | PT | CC CC inhibits the adherence of platelets to leukocytes. The fusion polypeptide CC is useful for treating a disorder associated with platelet activation e.g. ischaemic heart disease, acute myocardial infarction, stroke, venous |
| 17   | 1526   | 53.8        | 293    | 1 AAP91368 | Aap91368 45 kDa am | XX | CC CC  |
| 18   | 1521.5   | 53.6        | 302    | 5 ABB78241 | Abb78241 Amino aci | XX |  |
| 19   | 1521.5   | 53.6        | 610    | 2 AAR89436 | Aar89436 Mutated P | PS |  |
| 20   | 1521.5   | 53.6        | 610    | 2 AAW18201 | AAw18201 Platelet  | XX |  |
| 21   | 1520   | 53.5        | 290    | 5 ABB78245 | Abb78245 Amino aci | XX |  |
| 22   | 1518.5   | 53.5        | 610    | 2 AAR51116 | Aar51116 Platelet  | CC |  |
| 23   | 1514.5   | 53.3        | 610    | 2 AAR56664 | Aar56664 Mutant pl | CC |  |
| 24   | 1513.5   | 53.3        | 300    | 5 ABB78242 | Abb78242 Amino aci | CC |  |
| 25   | 1372   | 48.3        | 609    | 8 ADP76033 | ADP76033 AMIGO pol | CC |  |

CC thrombosis, atherosclerosis, arterial thrombosis or unstable angina. It can also be used to treat vascular conditions associated with vascular inflammation, thrombosis, and angioplasty-related restenosis

XX Sequence 531 AA;

Query Match 100.0%; Score 2819; DB 5; Length 531;  
Best Local Similarity 100.0%; Pred. No. 6.7e-205;  
Matches 531; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Db 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Db 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Qy 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120

Db 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120

Db 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180

Db 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180

Qy 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240

Db 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240

Qy 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCPTLGDEGDTLDYDYPEEDT 300

Db 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCPTLGDEGDTLDYDYPEEDT 300

Qy 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360

Db 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360

Qy 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420

Db 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420

Qy 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480

Db 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480

Qy 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531

Db 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531

Qy 531

Db 531

PP 06-FEB-2002; 2002WO-US003549.  
XX PR 06-FEB-2001; 2001US-0266838P.

XX PA (GEN) GENETICS INST LLC.  
XX PI Shaw GD, Kumar R, Sako DS, McDonagh T, Sullivan FX;

XX DR WPI: 2002-657537/70.  
XX DR N-PSDB; ABQ78864.

XX PT New glycoprotein Ib alpha fusion polypeptides, useful for treating a disorder associated with platelet activation e.g. ischaemic heart disease, stroke, venous or arterial thrombosis or atherosclerosis.  
XX PT stroke, venous or arterial thrombosis or atherosclerosis.  
XX PS Claim 20; Page 3; 45pp; English.

XX CC The present sequence represents a fusion protein of glycoprotein 1B-alpha (GP1b) and an immunoglobulin (Ig) polypeptide. The fusion protein inhibits the adherence of platelets to leukocytes. The fusion polypeptide is useful for treating a disorder associated with platelet activation e.g. ischaemic heart disease, acute myocardial infarction, stroke, venous thrombosis, arterial thrombosis or unstable angina. It can also be used to treat vascular conditions associated with vascular inflammation, thrombosis, and angioplasty-related restenosis.

XX CC Sequence 531 AA;  
XX CC Claim 20; Page 3; 45pp; English.

Query Match 99.6%; Score 2829; DB 5; Length 531;  
Best Local Similarity 99.6%; Pred. No. 3.8e-204;  
Matches 529; Conservative 1; Mis matches 1; Indels 0; Gaps 0;

Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60  
Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60  
Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Qy 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120  
Qy 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120

Qy 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180  
Qy 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180

Qy 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240  
Qy 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240

Qy 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCP TLGDEGDTLDYDYPEEDT 300  
Qy 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCP TLGDEGDTLDYDYPEEDT 300

Qy 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360  
Qy 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360

Qy 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420  
Qy 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420

Qy 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480  
Qy 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480

Qy 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531  
Qy 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531

Qy 531

XX PR 06-FEB-2002; 2002WO-US003549.  
XX PR 06-FEB-2001; 2001US-0266838P.

XX PA (GEN) GENETICS INST LLC.  
XX PI Shaw GD, Kumar R, Sako DS, McDonagh T, Sullivan FX;

XX DR WPI: 2002-657537/70.  
XX DR N-PSDB; ABQ78864.

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XX CC The present sequence represents a fusion protein of glycoprotein 1B-alpha (GP1b) and an immunoglobulin (Ig) polypeptide. The fusion protein inhibits the adherence of platelets to leukocytes. The fusion polypeptide is useful for treating a disorder associated with platelet activation e.g. ischaemic heart disease, acute myocardial infarction, stroke, venous thrombosis, arterial thrombosis or unstable angina. It can also be used to treat vascular conditions associated with vascular inflammation, thrombosis, and angioplasty-related restenosis.

XX CC Sequence 531 AA;  
XX CC Claim 20; Page 3; 45pp; English.

Query Match 99.6%; Score 2829; DB 5; Length 531;  
Best Local Similarity 99.6%; Pred. No. 3.8e-204;  
Matches 529; Conservative 1; Mis matches 1; Indels 0; Gaps 0;

Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60  
Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60  
Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Qy 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120  
Qy 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120

Qy 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180  
Qy 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180

Qy 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240  
Qy 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240

Qy 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCP TLGDEGDTLDYDYPEEDT 300  
Qy 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCP TLGDEGDTLDYDYPEEDT 300

Qy 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360  
Qy 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360

Qy 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420  
Qy 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420

Qy 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480  
Qy 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480

Qy 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531  
Qy 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531

Qy 531

XX PR 06-FEB-2002; 2002WO-US003549.  
XX PR 06-FEB-2001; 2001US-0266838P.

XX PA (GEN) GENETICS INST LLC.  
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XX DR N-PSDB; ABQ78864.

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XX CC Sequence 531 AA;  
XX CC Claim 20; Page 3; 45pp; English.

Query Match 99.6%; Score 2829; DB 5; Length 531;  
Best Local Similarity 99.6%; Pred. No. 3.8e-204;  
Matches 529; Conservative 1; Mis matches 1; Indels 0; Gaps 0;

Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60  
Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60  
Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Qy 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120  
Qy 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120

Qy 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180  
Qy 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180

Qy 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240  
Qy 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240

Qy 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCP TLGDEGDTLDYDYPEEDT 300  
Qy 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCP TLGDEGDTLDYDYPEEDT 300

Qy 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360  
Qy 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360

Qy 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420  
Qy 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420

Qy 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480  
Qy 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480

Qy 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531  
Qy 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531

Qy 531

XX PR 06-FEB-2002; 2002WO-US003549.  
XX PR 06-FEB-2001; 2001US-0266838P.

XX PA (GEN) GENETICS INST LLC.  
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XX DR WPI: 2002-657537/70.  
XX DR N-PSDB; ABQ78864.

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XX CC Sequence 531 AA;  
XX CC Claim 20; Page 3; 45pp; English.

Query Match 99.6%; Score 2829; DB 5; Length 531;  
Best Local Similarity 99.6%; Pred. No. 3.8e-204;  
Matches 529; Conservative 1; Mis matches 1; Indels 0; Gaps 0;

Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60  
Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60  
Qy 1 MPLLLLLLPSLPLPHPICEVKASHLEVNCDKRNLTAIPDLPKDTTILHSENLLY 60

Qy 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120  
Qy 61 TFSLATLMPYTRLTLQNLDRCELTKLQVDTLPVIGTLILSHNQLOSLPLGOTLPALTY 120

Qy 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180  
Qy 121 LDVSPNRLTSPLGAIRLQLQBLQELYLGKGNBLKLTQPLPGLITPTPKLEKLSANNNLTEUP 180

Qy 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240  
Qy 181 AGLLNGLENLDLQLQNSLYTIPKGFFGSHLPPAFLHNPMVLCENCELYFRMLQDNA 240

Qy 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCP TLGDEGDTLDYDYPEEDT 300  
Qy 241 ENVYWWKQVVDVKAVTSNVASVQCDNSDKEPVVYKPGKGCP TLGDEGDTLDYDYPEEDT 300

Qy 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360  
Qy 301 EGDKVPRHTCPCPKPAPEALGAPSFLFPPKPKDTLMISRTPEVTCVYVVSHEDEPKVKN 360

Qy 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420  
Qy 361 WYVDGYEVNVAKTKEPQEYQNSTYRVVSVTLHQDWLNGKEYKCKVSKNALKALPYIERTI 420

Qy 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480  
Qy 421 SKAKGQPREPQVYTLPPSREEMTQNSLCLVKGYPSPDIAVEWESNGOPENNYKTPPP 480

Qy 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531  
Qy 481 VLDSGDSFLSFYLSKLTVDKSRMROQGNVFSCSYTMHEALTHNHYTQKSLSSLSPGK 531

Qy 531

XX PR 06-FEB-2002; 2002WO-US003549.  
XX PR 06-FEB-2001







XX A method has been developed for the detection of binding between the von  
 CC Willebrand factor and glycoprotein Ib or of the binding inhibition, in  
 CC which the von Willebrand factor immobilised in a reactor reacts with  
 CC glycoprotein Ib in the presence of a binding inducer to promote binding  
 CC between the von Willebrand factor and glycoprotein Ib. This method is for  
 CC the detection of glykokallidin as a means of thrombotic disease diagnosis  
 CC e.g. for cardiac infarction and cerebral embolism, and also for screening  
 CC substances with anti-thrombotic activity for the prevention and treatment  
 CC of thrombotic diseases. The method is direct, convenient and  
 CC quantitative, with reproducibility, and there is no need to construct a  
 CC monoclonal antibody for the assay. The present sequence is a human  
 CC glycoprotein Ib/mouse immunoglobulin Gamma 1 Fc chimeric protein from the  
 CC present invention. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 562 AA;

Query Match 84.9%; Score 2411.5; DB 3; Length 562;  
 Best Local Similarity 79.5%; Pred. No. 1.1e-172;  
 Matches 449; Conservative 40; Mismatches 39; Indels 37; Gaps 4;

Qy 1 MPLLLLLLPSLPLSPHPICEVKASHLEVNCDRNLTAIPDLPKDITLHLSENLY 60

Db 1 MPLLLLLLPSLPLSPHPICEVKASHLEVNCDRNLTAIPDLPKDITLHLSENLY 60

Qy 61 TFSLATLMPTRLQLNLRECEITLKLQDGTLPLVGLTDLISHNQQLSLPLGQTLPA 120

Db 61 TFSLATLMPTRLQLNLRECEITLKLQDGTLPLVGLTDLISHNQQLSLPLGQTLPA 120

Qy 121 LDVSPNRLTSLPLGAIRLRLGFLQELQYLGKGNELKLTLPGLLITPTPKLEKSLANNNLTELP 180

Db 121 LDVSPNRLTSLPLGAIRLRLGFLQELQYLGKGNELKLTLPGLLITPTPKLEKSLANNNLTELP 180

Qy 181 AGLLNGLENIDTLLQIENSLYTIPKGFFGSHLPPAFLHNPNWLNCNCELYFRLWLDNA 240

Db 181 AGLLNGLENIDTLLQIENSLYTIPKGFFGSHLPPAFLHNPNWLNCNCELYFRLWLDNA 240

Qy 241 ENVYWKQVQDYKATISNVASVQCDNSDKSPVYKPGKCGPTLQEDGDTDLYDYPEEDT 300

Db 241 ENVYWKQVQDYKATISNVASVQCDNSDKSPVYKPGKCGPTLQEDGDTDLYDYPEEDT 300

Qy 301 EGDKYR--PHT----- 326

Db 301 EGDKYRATRTVVKFPTKAHTTPWGLFYSWSTASLDVPRDGCKFCITCPB--VSSVFI 357

Qy 327 FPPKPKDTLMSLRSRTPETVTVVYDHEPDKFENWVAKTKREEQNSTYRV 386

Db 358 FPPKPKDTLMSLRSRTPETVTVVYDHEPDKFENWVAKTKREEQNSTYRV 386

Qy 387 VSVLTVLHQDWLNGKEYKCKVSNKALPVPIEKTKAKGQPREPQVYTLPPSREEMTKHQ 446

Db 418 VSELPIMHODWLNGKEFKCRNSAAPPAPIEKTKAKGQPREPQVYTLPPSREEMTKHQ 477

Qy 447 VSLTCVLRGVFPSDIAVEWEENGOPENNNYKTPVPLDSDSFPLFLSKLTVDSRQQGNY 506

Db 478 VSLTCMIDTFPEDIITVQWINGQAPALENYYKNTQIMDTSYFVYSKLNVQKSWEAGNT 537

Qy 507 FSCSYNHEALHNHYTOKSLSLSPGK 531

Db 538 FTCVSLHEGLNHATEXLSLSPGK 562

RESULT 8

AY49935 ID AAY49935 standard: protein; 568 AA.

XX AC AAY49935;

XX DT 12-SEP-2003 (revised)

XX DT 01-FEB-2000 (first entry)

DB Human glycoprotein Ib/mouse IgG2aFc chimeric protein #2.

XX

KW Glycoprotein Ib; glykokallidin; detection; antithrombotic; binding;  
 KW von Willebrand factor; boottocetin; chimeric protein; immunoglobulin;  
 KW thrombotic disease; diagnosis; cardiac infarction; cerebral embolism.  
 XX Homo sapiens.  
 OS Mus musculus.  
 OS Chimeric.  
 XX  
 Key FH Location/Qualifiers  
 Peptide FT 1..16  
 Label= signal  
 Protein FT 17..568  
 Label= Human\_glycoprotein\_Ib/mouse\_IgG2aFc\_chimeric  
 protein FT  
 XX  
 PN WO954360-A1.  
 XX  
 PD 28-OCT-1999.  
 PP 13-JAN-1999;  
 XX  
 PR 23-APR-1998;  
 98JP-00113962.  
 PA (AJIN) AJINOMOTO CO INC.  
 PI Fukuchi N, Putaki F, Kito M, Sato S, Kajura T, Ono Y, Ishii K;  
 PI Tanaka A, Shinozaki J, Jojima Y;  
 DR WPI; 2000-013233/01.  
 DR N-PDB; AAZ35706.

XX  
 PT Direct quantitative detection of glykokallidin with immobilized von  
 PT Willebrand factor to bond with chimeric protein via inhibiting  
 PT glycoprotein Ib binding, for diagnosis of thrombotic diseases and  
 PT screening anti-thrombotic substances.  
 XX  
 PS Example 1: Page 77-79; 83pp; Japanese.  
 XX  
 CC A method has been developed for the detection of binding between the von  
 CC Willebrand factor and glycoprotein Ib or of the binding inhibition, in  
 CC which the von Willebrand factor immobilised in a reactor reacts with  
 CC glycoprotein Ib in the presence of a binding inducer to promote binding  
 CC between the von Willebrand factor and glycoprotein Ib. This method is for  
 CC the detection of glykokallidin as a means of thrombotic disease diagnosis  
 CC e.g. for cardiac infarction and cerebral embolism, and also for  
 CC substances with anti-thrombotic activity for the prevention and treatment  
 CC of thrombotic diseases. The method is direct, convenient and  
 CC quantitative, with reproducibility, and there is no need to construct a  
 CC monoclonal antibody for the assay. The present sequence represents a  
 CC human glycoprotein Ib/mouse immunoglobulin Gamma 2a Fc chimeric protein  
 CC from the present invention. (Updated on 12-SEP-2003 to standardise OS  
 CC field)  
 XX  
 SQ Sequence 568 AA;  
 XX  
 Query Match 83.9%; Score 2381.5; DB 3; Length 568;  
 Best Local Similarity 79.4%; Pred. No. 2e-170; Mis matches 51; Indels 37; Gaps 3;  
 Matches 451; Conservative 29;  
 Qy 1 MPLLLLLLPSLPLSPHPICEVKASHLEVNCDRNLTAIPDLPKDITLHLSENLY 60  
 Db 1 MPLLLLLLPSLPLSPHPICEVKASHLEVNCDRNLTAIPDLPKDITLHLSENLY 60  
 XX  
 Qy 61 TFSLTLMPTRLQLNLRECEITLKLQDGTLPLVGLTDLISHNQQLSLPLGQTLPA 120  
 Db 61 TFSLTLMPTRLQLNLRECEITLKLQDGTLPLVGLTDLISHNQQLSLPLGQTLPA 120  
 XX  
 Qy 121 LDVSPNRLTSLPLGAIRLRLGFLQELQYLGKGNELKLTLPGLLITPTPKLEKSLANNNLTELP 180  
 Db 121 LDVSPNRLTSLPLGAIRLRLGFLQELQYLGKGNELKLTLPGLLITPTPKLEKSLANNNLTELP 180  
 XX  
 Qy 181 AGLLNGLENIDTLLQIENSLYTIPKGFFGSHLPPAFLHNPNWLNCNCELYFRLWLDNA 240  
 Db 181 AGLLNGLENIDTLLQIENSLYTIPKGFFGSHLPPAFLHNPNWLNCNCELYFRLWLDNA 240



|           |  |                  |   |   |
|-----------|--|------------------|---|---|
| XX        | 28-FEB-2003;   | 2003WO-US006025. | XX  | ID ADJ6864 standard; protein; 626 AA.                                     |
| PF        |  |                  | XX  |   |
| XX        | 01-MAR-2002;   | 2002US-036119P.  | AC  | ADJ68624;   |
| PR        |  |                  | XX  |   |
| XX        |  |                  | DT  | 06-MAY-2004 (first entry)   |
| PA        |  |                  | XX  | Human heat mitochondrial protein as a therapeutic target SeqID430.        |
| XX        |  |                  | XX  | mitochondrial; human; screening assay; diabetes mellitus;                 |
| PT        |  |                  | XX  | Huntington's disease; osteoarthritis;                                     |
| XX        |  |                  | KW  | Leber's hereditary optic neuropathy; LHON;                                |
| DR        | WPI; 2003-12540/76.  |                  | KW  | mitochondrial encephalopathy lactic acidosis and stroke; MELAS;           |
| DR        | N-NSDB; ADE69150.  |                  | KW  | myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;              |
| XX        |  |                  | KW  | neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  |
| PR        | Identifying a candidate p53 pathway modulating agent for treating e.g.,            |                  | KW  | osteopathic; ophthalmological; cytosstatic.                               |
| PR        | cancer by contacting an assay system comprising a MP53 polypeptide or              |                  | XX  |   |
| PR        | nucleic acid with a test agent and detecting a test agent-biased                   |                  | OS  |   |
| XX        | activity.  |                  | Homo sapiens.   |   |
| PS        | Example; SEQ ID NO 64; 406pp; English.   |                  | XX  |   |
| XX        |  |                  | PN  | WO2003087768-A2.  |
| CC        | The present invention describes a method for identifying a candidate p53           |                  | XX  |   |
| CC        | pathway modulating agent, which comprises (a) providing an assay system            |                  | PD  | 23-OCT-2003.  |
| CC        | comprising a p53 (modulator) polypeptide or nucleic acid or its                    |                  | XX  | 04-APR-2003;  |
| CC        | fragment or derivative; (b) contacting the assay system with a test agent          |                  | PP  | 2003WO-US010870.  |
| CC        | under conditions where the system provides a reference activity except in          |                  | XX  |   |
| CC        | the presence of the test agent; and (c) detecting a test agent-biased activity and |                  | PR  | 12-APR-2002;  |
| CC        | the reference activity identifies the test agent as a candidate p53                |                  | PR  | 2002US-0372843P.  |
| CC        | pathway modulating agent. Also described: (1) modulating the p53 pathway           |                  | PR  | 17-JUN-2002;  |
| CC        | of a cell; (2) modulating the p53 pathway in a mammalian cell; and (3)             |                  | PR  | 20-JUN-2002;  |
| CC        | diagnosing a disease in a patient. MP53 has cytosstatic activity, and can          |                  | XX  | 2002US-0389987P.  |
| CC        | be used in gene therapy. The method is useful for identifying a candidate          |                  | XX  | 2002US-0412418P.  |
| CC        | p53 pathway modulating agent for preparing a composition for diagnosing            |                  | XX  |   |
| CC        | or treating e.g., cancer. The present sequence represents a human MP53             |                  | XX  |   |
| CC        | protein, which is used in the exemplification of the present invention.            |                  | XX  |   |
| XX        |  |                  | XX  | (MITO-) MITOKOR.  |
| CC        |  |                  | PA  | (BUCK-) BUCK INST AGE RES.  |
| CC        |  |                  | XX  | PA (BUCK-) BUCK INST AGE RES.   |
| CC        |  |                  | XX  | Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;               |
| CC        |  |                  | PI  | Warnock DE;   |
| CC        |  |                  | PI  |   |
| CC        |  |                  | XX  |   |
| CC        |  |                  | XX  | WPI; 2003-845369/78.  |
| CC        |  |                  | XX  |   |
| CC        |  |                  | XX  | Identifying a mitochondrial target for drug screening assays and for      |
| CC        |  |                  | PT  | treating diseases associated with altered mitochondrial function,         |
| CC        |  |                  | PT  | comprises detecting a modified polypeptide in a sample and correlating    |
| CC        |  |                  | PT  | with the disease.   |
| CC        |  |                  | XX  | Claim 1; SEQ ID NO 430; 180pp; English.                                   |
| CC        |  |                  | XX  | This invention relates to novel mitochondrial targets that can be used    |
| CC        |  |                  | CC  | for therapeutic intervention in treating a disease associated with        |
| CC        |  |                  | CC  | altered mitochondrial function. Specifically, it refers to a method for   |
| CC        |  |                  | CC  | identifying proteins of the human heart mitochondrial proteome that are   |
| CC        |  |                  | CC  | useful for drug screening assays, as well as therapeutic targets. The     |
| CC        |  |                  | CC  | present invention describes a method for identifying such proteins that   |
| CC        |  |                  | CC  | can be used in the treatment of various diseases associated with altered  |
| CC        |  |                  | CC  | mitochondrial function including diabetes mellitus, Huntington's disease, |
| CC        |  |                  | CC  | osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial |
| CC        |  |                  | CC  | encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy     |
| CC        |  |                  | CC  | raged red fibre syndrome (MERRF) or cancer. Accordingly, these            |
| CC        |  |                  | CC  | compositions have neuroprotective, nootropic, antidiabetic,               |
| CC        |  |                  | CC  | antiarthritic, osteopathic, ophthalmological and                          |
| CC        |  |                  | CC  | cytostatic activities. This polypeptide sequence is a human heart         |
| CC        |  |                  | CC  | mitochondrial protein of the invention.                                   |
| XX        |  |                  | XX  | Sequence 626 AA;  |
| QY        | 1 MPILLILLPLSPHPICEVSKVASHLEVNCDKRNATLPDLPKTTIHLSENLY 60                           |                  | QY  | Sequence 626 AA;  |
| Db        | 1 MPILLILLPLSPHPICEVSKVASHLEVNCDKRNATLPDLPKTTIHLSENLY 60                           |                  | QY  | 1 MPILLILLPLSPHPICEVSKVASHLEVNCDKRNATLPDLPKTTIHLSENLY 60                  |
| QY        | 61 TFSLATLMPYTRTQLNLDRCELTKLQDGTLVQLGTDLDSHNOQLPQLGQTLPALTV 120                    |                  | Db  | 1 MPILLILLPLSPHPICEVSKVASHLEVNCDKRNATLPDLPKTTIHLSENLY 60                  |
| Db        | 61 TFSLATLMPYTRTQLNLDRCELTKLQDGTLVQLGTDLDSHNOQLPQLGQTLPALTV 120                    |                  | QY  | 56.9%; Score 1615.5; DB 7; Length 626;                                    |
| QY        | 121 LDYFSNRNTSLPLGALRGIGELQDLYLGKNEKLTKLPPGLTTPPKLDSLANNNLTEL 180                  |                  | Best Local Similarity 84.2%; Pred. No. 1e-112;                |   |
| Db        | 121 LDYFSNRNTSLPLGALRGIGELQDLYLGKNEKLTKLPPGLTTPPKLDSLANNNLTEL 180                  |                  | Matches 319; Conservative 5; Mismatches 20; Indels 35; Gaps 5 |   |
| QY        | 181 AGLINGLENLDTLQLQENSLTYTPKGFGSHLPPAFTHGNPLCNCIILYPRWLQDNA 240                   |                  | Query Match 56.9%; Score 1615.5; DB 7; Length 626;            |   |
| Db        | 181 AGLINGLENLDTLQLQENSLTYTPKGFGSHLPPAFTHGNPLCNCIILYPRWLQDNA 240                   |                  | Best Local Similarity 84.2%; Pred. No. 1e-112;                |   |
| QY        | 241 ENTYWKQYDVKAVTSVAVSYQCDNSDKEPVYKYPGKGCPYLGEDEGTLDLYYPEBDT 300                  |                  | Matches 319; Conservative 5; Mismatches 20; Indels 35; Gaps 5 |   |
| Db        | 241 ENYVWKQYDVKAVTSVAVSYQCDNSDKEPVYKYPGKGCPYLGEDEGTLDLYYPEBDT 300                  |                  | Query Match 56.9%; Score 1615.5; DB 7; Length 626;            |   |
| QY        | 301 EGDKYR-----PHTCP-----POPA---PEALGAPSYVFLFPFK-- 330                             |                  | Best Local Similarity 84.2%; Pred. No. 1e-112;                |   |
| Db        | 301 EGDKYRATRTVVKPFTKAHTTTPGLFYSWSTASLDSQMPSSLHPTQESTKEQTTPPRWT 360                |                  | Matches 319; Conservative 5; Mismatches 20; Indels 35; Gaps 5 |   |
| QY        | 331 PKDTL-----MISSTPEV 344   |                  | Query Match 56.9%; Score 1615.5; DB 7; Length 626;            |   |
| Db        | 361 PNFTLHMESSITFSKTPKST 379   |                  | Best Local Similarity 84.2%; Pred. No. 1e-112;                |   |
| RESULT 11 | 61 TFSLATLMPYTRTQLNLDRCELTKLQDGTLVQLGTDLDSHNOQLPQLGQTLPALTV 120                    |                  | Matches 319; Conservative 5; Mismatches 20; Indels 35; Gaps 5 |   |
| Db        | 61 TFSLATLMPYTRTQLNLDRCELTKLQDGTLVQLGTDLDSHNOQLPQLGQTLPALTV 120                    |                  | Query Match 56.9%; Score 1615.5; DB 7; Length 626;            |   |

Qy 121 LDVSFRNLTSPLIGALRGIGELOEYLKGNEKLTKLPPSLITPTPKGEKLISLANNNLTELP 180  
 Db 121 LDVSFRNLTSPLIGALRGIGELOEYLKGNEKLTKLPPSLITPTPKGEKLISLANNNLTELP 180

Qy 181 AGLINGLENLDTLQLQNSLYTIPKGFFGSHLIPFAFLHGNPMLCNECBLIFPRWLQDNA 240  
 Db 181 AGLINGLENLDTLQLQNSLYTIPKGFFGSHLIPFAFLHGNPMLCNECBLIFPRWLQDNA 240

Qy 241 ENYVWKQGVYDVKAVTNTAVSQCDNSPKFVKPYKPGKCPPLGDEGDTDLVYYPEDT 300  
 Db 241 ENYVWKQGVYDVKAVTNTAVSQCDNSPKFVKPYKPGKCPPLGDEGDTDLVYYPEDT 300

Qy 301 EGDKVVR-----BHTCP-----EGDKVVR-----BHTCP-----EGDKVVR-----BHTCP----- 330  
 Db 301 EGDKVRAVTRTVVKFPTKAHTTPMGLFYSWSTASLDQMSQPSLHPTQESTKEQTTPRWT 360

Qy 331 PKDTL-----MISRTPEVY 344  
 Db 361 PNFTLHMESETFSKTPKST 379

## RESULT 12

ADH40324

ADH40324 standard; protein; 626 AA.

AC ADH40324;

XX XX

DT 11-MAR-2004 (first entry)

DS Human platelet glycoprotein IB alpha chain precursor CD42b.

KW human; platelet glycoprotein IB alpha chain precursor; CD42b; cytostatic; vaccine; SNP profile; cancer; leukaemia.

XX OS Homo sapiens.

XX PN WO2003106692-A2.

XX PD 24-DEC-2003.

XX XX

PF 13-JUN-2003; 2003WO-EP006251.

XX PR 13-JUN-2002; 2002EP-00013423.

XX PA (MERÈ ) MERCK PATENT GMBH.

XX PI Strittmatter W, Moll H;

XX DR WPI; 2004-082200/08.

XX PT Providing allelic variant epitope of protein based on single nucleotide polymorphism by defining target protein, screening database of protein, identifying, selecting allelic variant protein, creating variant epitopes.

XX PS Example 4; Page 67; 119pp; English.

XX XX

PA 22-DEC-2003; 2003WO-US040978.

XX PR 20-DEC-2002; 2002US-0434778P.

XX PR 10-MAR-2003; 2003US-0453135P.

XX PR 30-APR-2003; 2003US-046612P.

XX PR 23-SEP-2003; 2003US-050455P.

XX PA (APPL ) APPLERA CORP.

XX PI Cargill M, Devlin JJ, Iakoubova O;

XX DR WPI; 2004-533949/51.

DR N-PSDB; ADG39005.

XX PT Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Qy sequence is used in the exemplification of the invention.

CC XX Sequence 626 AA;

SQ Sequence 626 AA;  
 Query Match 56.9%; Score 1615.5; DB 8; Length 626;  
 Best Local Similarity 84.2%; Pred. No. 1e-112;  
 Matches 5; Mismatches 20; Indels 35; Gaps 5;Qy 1 MPILLIPLLSPPLHHPICVSKVASHLEYNCDRKNTALPDLPKDTTILHLSNENLY 60  
 Db 1 MPILLIPLLSPPLHHPICVSKVASHLEYNCDRKNTALPDLPKDTTILHLSNENLY 60Qy 61 TFSLATATMPYTRLTLQNLDRCLTLQVGDGTLPVLTGLTDLSHNOQSLPLUGOTLPALTV 120  
 Db 61 TFSLATATMPYTRLTLQNLDRCLTLQVGDGTLPVLTGLTDLSHNOQSLPLUGOTLPALTV 120Qy 61 TFSLATATMPYTRLTLQNLDRCLTLQVGDGTLPVLTGLTDLSHNOQSLPLUGOTLPALTV 180  
 Db 61 TFSLATATMPYTRLTLQNLDRCLTLQVGDGTLPVLTGLTDLSHNOQSLPLUGOTLPALTV 180Qy 121 LDVSFRNLTSPLIGALRGIGELOEYLKGNEKLTKLPGGLTPPKLFEKLISLANNNLTELP 180  
 Db 121 LDVSFRNLTSPLIGALRGIGELOEYLKGNEKLTKLPGGLTPPKLFEKLISLANNNLTELP 180Qy 121 LDVSFRNLTSPLIGALRGIGELOEYLKGNEKLTKLPGGLTPPKLFEKLISLANNNLTELP 240  
 Db 121 LDVSFRNLTSPLIGALRGIGELOEYLKGNEKLTKLPGGLTPPKLFEKLISLANNNLTELP 240Qy 181 AGLINGLENLDTLQLQNSLYTIPKGFFGSHLIPFAFLHGNPMLCNECBLIPRWLQDNA 240  
 Db 181 AGLINGLENLDTLQLQNSLYTIPKGFFGSHLIPFAFLHGNPMLCNECBLIPRWLQDNA 240Qy 241 ENYVWKQGVYDVKAVTNTAVSQCDNSPKFVKPYKPGKCPPLGDEGDTDLVYYPEDT 300  
 Db 241 ENYVWKQGVYDVKAVTNTAVSQCDNSPKFVKPYKPGKCPPLGDEGDTDLVYYPEDT 300Qy 241 ENYVWKQGVYDVKAVTNTAVSQCDNSPKFVKPYKPGKCPPLGDEGDTDLVYYPEDT 360  
 Db 241 ENYVWKQGVYDVKAVTNTAVSQCDNSPKFVKPYKPGKCPPLGDEGDTDLVYYPEDT 360Qy 241 ENYVWKQGVYDVKAVTNTAVSQCDNSPKFVKPYKPGKCPPLGDEGDTDLVYYPEDT 399  
 Db 241 ENYVWKQGVYDVKAVTNTAVSQCDNSPKFVKPYKPGKCPPLGDEGDTDLVYYPEDT 399Qy 301 EGDKVVR-----BHTCP-----EGDKVVR-----BHTCP-----EGDKVVR-----BHTCP----- 330  
 Db 301 EGDKVVR-----BHTCP-----EGDKVVR-----BHTCP-----EGDKVVR-----BHTCP----- 360Qy 331 PKDTL-----MISRTPEVY 344  
 Db 361 PNFTLHMESETFSKTPKST 379RESULT 13  
 ADQ39833

ID ADQ39833 standard; protein; 626 AA.

XX AC ADQ39833;

XX DT 18-NOV-2004 (first entry)

XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.

XX PN WO2004058052-A2.

XX PD 15-JUL-2004.

XX XX Homo sapiens.

XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.XX XX XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1496.  
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.  
 XX OS Homo sapiens.

XX Claim 10; SEQ ID NO 1496; 145PP; English.

XX The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

XX Sequence 626 AA;

Query Match 56.9%; Score 1615.5; DB 8; Length 626; Best Local Similarity 84.2%; Pred. No. 1e-112; Matches 319; Conservative 5; Mismatches 20; Indels 35; Gaps 5;

Qy 1 M P L L L L L L S P L H P I C V S K Y A S H L E V N C D R N L T A P P D L P K D T T I L H S E N L Y 60  
Db 1 M P L L L L L L P S P L H P I C V S K Y A S H L E V N C D R N L T A P P D L P K D T T I L H S E N L Y 60  
Qy 61 T F S L A T I M P Y T R T I Q N L D R C B L T K L Q V D G T L P V G I T L D L S H N Q L Q S L P I L G Q T L P A L T V 120  
Db 61 T F S L A T I M P Y T R T I Q N L D R C B L T K L Q V D G T L P V G I T L D L S H N Q L Q S L P I L G Q T L P A L T V 120

Qy 121 L D V S F R L T S I P L G A R I R G G H L Q E Y L K G N E L K T L P P G L I T P T P K L E K I S L A N N N L T E P 180  
Db 121 L D V S F R L T S I P L G A R I R G G H L Q E Y L K G N E L K T L P P G L I T P T P K L E K I S L A N N N L T E P 180

Qy 181 A G L I N G L E N L D T I L L Q E N S L Y T I P G F R G S H L I P P A F L H G N P M I C N C E I Y F R M I Q D N A 240  
Db 181 A G L I N G L E N L D T I L L Q E N S L Y T I P G F R G S H L I P P A F L H G N P M I C N C E I Y F R M I Q D N A 240

Qy 241 E N V Y W K Q V D V K A T S N V A S Q C D N S D K F P V K Y P G K G C P T L G D E G D T D Y D Y P E E D T 300  
Db 241 E N V Y W K Q V D V K A T S N V A S Q C D N S D K F P V K Y P G K G C P T L G D E G D T D Y D Y P E E D T 300

Qy 301 E G D K V T R - - - - - P H T Q T - - - - - P C P A - - - P R A L G A P S V E F P P K - - 330  
Db 301 E G D K V T R T V V K F P T K A H T P W G L F Y S W T A S L D S Q M P S S L H P T Q E S T K E Q T T P P R V T 360

Qy 331 P K D T L - - - M I S R T P E V T 344  
Db 361 P N F T L H E M S T I T F S K T P K S T 379

XX DE. Amino acid sequence of glycoprotein 1B-alpha polypeptide GP1b290/2V.

XX Glycoprotein 1B-alpha; GP1b; immunoglobulin Ig; platelet adherence; leucocyte; platelet activation; ischaemic heart disease; acute myocardial infarction; stroke; venous thrombosis; atherosclerosis; arterial thrombosis; angina; vascular condition; vascular inflammation; thrombosis; angioplasty; restenosis.

XX Unidentified.

OS WO200263003-A2.

XX PD 15-AUG-2002.

PP 06-FEB-2002; 2002WO-US003549.

XX PR 06-FEB-2001; 2001US-0266838P.

XX PA (GEMY ) GENETICS INST LLC.

PI Shaw GD, Kumar R, Sako DS, Mcdonagh T, Sullivan FX;

XX DR 2002-657537/70.

XX PT New glycoprotein Ib alpha fusion Polypeptides, useful for treating a disorder associated with platelet activation e.g. ischemic heart disease, stroke, venous or arterial thrombosis or atherosclerosis.

XX PS Disclosure; Page 11; 45pp; English.

XX CC ABB8240-45 represent glycoprotein 1B-alpha (GP1b) polypeptides, which are used to produce fusion proteins with an immunoglobulin (Ig) polypeptide. The fusion proteins inhibit the adherence of platelets to leucocytes. The fusion polypeptides are useful for treating a disorder associated with platelet activation e.g. ischaemic heart disease, acute myocardial infarction, stroke, venous thrombosis, atherosclerosis, arterial thrombosis or unstable angina. They can also be used to treat vascular conditions associated with vascular inflammation, thrombosis, and angioplasty-related restenosis.

XX SQ Sequence 290 AA;

Query Match 54.1%; Score 1536; DB 5; Length 290; Best Local Similarity 10.0%; Pred. No. 3.6e-107; Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 H P I C V S K Y A S H L E V N C D R N L T A P P D L P K D T T I L H S E N L Y T F S L A T I M P Y T R T L Q T L Q 76  
Db 1 H P I C V S K Y A S H L E V N C D R N L T A P P D L P K D T T I L H S E N L Y T F S L A T I M P Y T R T L Q T L Q 60

Qy 77 N L D R C B L T K L Q V D G T L P V G I T L D I S H N Q L Q S L P I L G Q T L P A L T V D S F R L T S P L G A L 136  
Db 61 N L D R C B L T K L Q V D G T L P V G I T L D I S H N Q L Q S L P I L G Q T L P A L T V D S F R L T S P L G A L 120

Qy 137 R G L G L Q E L Y L K G N E L K T L P P G L I T P T P K L E K I S L A N N N L T E P G L I N G L E N L D T I L L Q 196  
Db 121 R G L G L Q E L Y L K G N E L K T L P P G L I T P T P K L E K I S L A N N N L T E P G L I N G L E N L D T I L L Q 180

Qy 197 E N S L Y T I P K G F P G S H L I P P A F L H G N P W L C N C E I Y F R M I Q D N A E N V T W K Q V D V Y K A V T 256  
Db 181 E N S L Y T I P K G F P G S H L I P P A F L H G N P W L C N C E I Y F R M I Q D N A E N V T W K Q V D V Y K A V T 240

Qy 257 S N V A S V Q C D N S D K F P V Y K T P G K G C P T L G D E G D T D Y D Y P E E D T G D K V R 306  
Db 241 S N V A S V Q C D N S D K F P V Y K T P G K G C P T L G D E G D T D Y D Y P E E D T G D K V R 290

RESULT 14  
ID ABB78244 standard; protein; 280 AA.  
XX AC ABB78244;  
XX DT 25-NOV-2002 (first entry)

RESULT 15  
ID ABB78240 standard; protein; 301 AA.  
XX AC ABB78240;  
XX DT ABB78240;

Search completed: May 24, 2005, 06:00:09  
 Job time : 167 secs

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XX 25-NOV-2002 (first entry)  
 XX DT Amino acid sequence of glycoprotein 1B-alpha polypeptide GP1b102.  
 XX KW Glycoprotein 1B-alpha; GP1b; immunoglobulin; Ig; platelet adherence;  
 XX leukocyte; platelet activation; stroke; venous thrombosis; ischaemic heart disease;  
 XX acute myocardial infarction; stroke; venous thrombosis; atherosclerosis;  
 XX arterial thrombosis; angina; vascular condition; vascular inflammation;  
 XX thrombosis; angioplasty; restenosis.  
 XX Unidentified.  
 OS  
 XX WO200261003-A2.  
 XX PD 15-AUG-2002.  
 XX PF 06-FEB-2002; 2002WO-US003549.  
 XX PR 06-FEB-2001; 2001US-0266838P.  
 XX PA (GEMY ) GENETICS INST LLC.  
 XX P1 Shaw GD, Kumar R, Sako DS, Mcdonagh T, Sullivan FX;  
 XX P2 DR 2002-657537/70.  
 XX PT New glycoprotein Ib alpha fusion polypeptides, useful for treating a  
 PT disorder associated with platelet activation e.g. ischemic heart disease,  
 PT stroke, venous or arterial thrombosis or atherosclerosis.  
 XX Disclosure; Page 10; 45pp; English.  
 XX CC AB7824-45 represent glycoprotein 1B-alpha (GP1b) polypeptides, which  
 CC are used to produce fusion proteins with an immunoglobulin (Ig)  
 CC polypeptide. The fusion proteins inhibit the adherence of platelets to  
 CC leukocytes. The fusion polypeptides are useful for treating a disorder  
 CC associated with platelet activation e.g. ischaemic heart disease, acute  
 CC myocardial infarction, stroke, venous thrombosis, atherosclerosis,  
 CC arterial thrombosis or unstable angina. They can also be used to treat  
 CC vascular conditions associated with vascular inflammation, thrombosis,  
 CC and angioplasty-related restenosis.  
 XX SQ Sequence 301 AA;

| Query | Match  | Score | Length |
|-------|--|-------|--------|
| Qy    | 17 HPICEVSKVASHLVEVNCDKRNLTAALPPDILPKDTTLHISENLYTFSIATLAMPYTRTLQ | 53.8% | 301;   |
| Qy    | 1 HPICEVSKVASHLVEVNCDKRNLTAALPPDILPKDTTLHISENLYTFSIATLAMPYTRTLQ  | 53    | 76     |
| Db    | 77 NLDRCELTQVQDGTLPLVGLTLDLHNQIQLSPILQGQTIPALTVDVSFRNLTSPLGAL    | 93.0% | 136    |
| Db    | 61 NLDRCELTQVQDGTLPLVGLTLDLHNQIQLSPILQGQTIPALTVDVSFRNLTSPLGAL    | 93    | 120    |
| Qy    | 137 RGIGBQEIYLYKGNEELKTLPPGLLPTPTKLEKLSLANNLTELPAGLNGLENLTLLQ    | 93.0% | 196    |
| Db    | 121 RGIGBQEIYLYKGNEELKTLPPGLLPTPTKLEKLSLANNLTELPAGLNGLENLTLLQ    | 93    | 180    |
| Qy    | 197 ENSLYTIPGFFGSHLLPFAFLHGNPNLQNCETLYFRRWLQDNAENTYVWQVQVDFKAVT  | 93    | 256    |
| Db    | 181 ENSLYTIPGFFGSHLLPFAFLHGNPNLQNCETLYFRRWLQDNAENTYVWQVQVDFKAVT  | 93    | 240    |
| Qy    | 257 SVAVQCDNSDKEPVYKPGKCPGPTLSDGDDTDLYYPEEDETEGDKVRPHTCPPCPA     | 93    | 316    |
| Db    | 241 SVAVQCDNSDKEPVYKPGKCPGPTLSDGDDTDLYYPEEDETEGDKVR-----         | 93    | 290    |
| Qy    | 317 EALGAPSYLEFPPK   | 93    | 330    |
| Db    | 291 ---ATRTWKFPTK  | 93    | 300    |

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: May 24, 2005, 06:00:18 ; Search time 136 Seconds (without alignments)  
1306.055 Million cell updates/sec

Title: US-10-068-426-5  
Pefect score: 2839  
Sequence: 1 MPULLLILPSPLHPIIC.....MHEALHNHYTQKSLSLSPGK 531

Scoring table: BLOSUM62  
Gapext 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:  
1: /cgn2\_6/\_ptodata/2/\_pubpa/\_US07\_PUBCOMB.pep/\*  
2: /cgn2\_6/\_ptodata/2/\_pubpa/\_PCT\_NEW\_PUB.pep/\*  
3: /cgn2\_6/\_ptodata/2/\_pubpa/\_US06\_NEWW\_PUB.pep/\*  
4: /cgn2\_6/\_ptodata/2/\_pubpa/\_US07\_NEW\_PUB.pep/\*  
5: /cgn2\_6/\_ptodata/2/\_pubpa/\_PCTUS\_PUBCOMB.pep/\*  
6: /cgn2\_6/\_ptodata/2/\_pubpa/\_US08\_NEW\_PUB.pep/\*  
8: /cgn2\_6/\_ptodata/2/\_pubpa/\_US08\_PUBCOMB.pep/\*  
9: /cgn2\_6/\_ptodata/2/\_pubpa/\_US09\_PUBCOMB.pep/\*  
10: /cgn2\_6/\_ptodata/2/\_pubpa/\_US09B\_PUBCOMB.pep/\*  
11: /cgn2\_6/\_ptodata/2/\_pubpa/\_US09C\_PUBCOMB.pep/\*  
12: /cgn2\_6/\_ptodata/2/\_pubpa/\_US09\_NEWW\_PUB.pep/\*  
13: /cgn2\_6/\_ptodata/2/\_pubpa/\_US10A\_PUBCOMB.pep/\*  
14: /cgn2\_6/\_ptodata/2/\_pubpa/\_US10B\_PUBCOMB.pep/\*  
15: /cgn2\_6/\_ptodata/2/\_pubpa/\_US10C\_PUBCOMB.pep/\*  
16: /cgn2\_6/\_ptodata/2/\_pubpa/\_US10D\_PUBCOMB.pep/\*  
17: /cgn2\_6/\_ptodata/2/\_pubpa/\_US10\_NEWW\_PUB.pep/\*  
18: /cgn2\_6/\_ptodata/2/\_pubpa/\_US11\_NEWW\_PUB.pep/\*  
19: /cgn2\_6/\_ptodata/2/\_pubpa/\_US60\_NEWW\_PUB.pep/\*  
20: /cgn2\_6/\_ptodata/2/\_pubpa/\_US60\_PUBCOMB.pep/\*

RESULT 1  
US-10-068-426-5

; Publication No. US20030091576A1  
; GENERAL INFORMATION:  
; APPLICANT: Shaw, Gray D.  
; APPLICANT: Sako, Dianne S.  
; APPLICANT: Kumar, Ravindra  
; APPLICANT: Sullivan, Francis  
; APPLICANT: McDonagh, Tom  
; TITLE OF INVENTION: Platlet Glycoprotein IB Alpha Fusion Polypeptides and  
; TITLE OF INVENTION: Methods of Use Thereof  
; FILE REFERENCE: 220058-503  
; CURRENT APPLICATION NUMBER: US/10/068,426  
; CURRENT FILING DATE: 2002-02-06  
; PRIOR APPLICATION NUMBER: 60/266,838  
; PRIOR FILING DATE: 2001-02-06  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 531  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (1)..(531)  
; OTHER INFORMATION: GPIb290/2V-Ig

US-10-068-426-5

Query Match 100 %; Score 2839; DB 14; Length 531;  
Best Local Similarity 100 %; Pred. No. 8e-201; Mismatches 0; Indels 0; Gaps 0;

1 MPILLLILPSPLHPIICYSKVASLHEVNCDFKRNLTALPPDLPKDTTILHLSNLLY 60  
Qy 1 MPILLLILPSPLHPIICYSKVASLHEVNCDFKRNLTALPPDLPKDTTILHLSNLLY 60  
Db 1 MPILLLILPSPLHPIICYSKVASLHEVNCDFKRNLTALPPDLPKDTTILHLSNLLY 60

Summaries

§  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score  | Query Match | Length | DB ID | Description        |
|------------|--------|-------------|--------|-------|--------------------|
| 1          | 2839   | 100.0       | 531    | 14    | US-10-068-426-5    |
| 2          | 2839   | 100.0       | 531    | 15    | US-10-068-758-1    |
| 3          | 2829   | 99.6        | 531    | 14    | US-10-068-426-4    |
| 4          | 2829   | 99.6        | 531    | 15    | US-10-068-758-4    |
| 5          | 2823   | 99.4        | 531    | 14    | US-10-068-426-6    |
| 6          | 2823   | 99.4        | 531    | 15    | US-10-068-758-6    |
| 7          | 2822.5 | 99.4        | 544    | 14    | US-10-068-426-3    |
| 8          | 2822.5 | 99.4        | 544    | 15    | US-10-068-758-3    |
| 9          | 2812.5 | 99.1        | 544    | 14    | US-10-068-426-1    |
| 10         | 2812.5 | 99.1        | 544    | 14    | US-10-068-426-2    |
| 11         | 2812.5 | 99.1        | 544    | 15    | US-10-068-758-2    |
| 12         | 2812.5 | 99.1        | 544    | 15    | US-10-068-758-5    |
| 13         | 1615.5 | 56.9        | 626    | 16    | US-10-408-765A-430 |



Qy 121 LDYSFNRLTSLPLGALRGIGELOBLYLKGNEELKTLPPGILTPTPKLEKLSSLANNNLTELP 180  
 Db 121 LDYSFNRLTSLPLGALRGIGELOBLYLKGNEELKTLPPGILTPTPKLEKLSSLANNNLTELP 180  
 Qy 181 AGLNGLENLDTLQENSLLTIPKGFPNSHLLPAFTLHGNPMLCNECEILYFRWLQDNA 240  
 Db 181 AGLNGLENLDTLQENSLLTIPKGFPNSHLLPAFTLHGNPMLCNECEILYFRWLQDNA 240  
 Qy 241 ENYVWQVQDVKAFTNSVASYQCDNSDKEPPTYKPKGCPPLGDEGSTDLDYYPEEDT 300  
 Db 241 ENYVWQVQDVKAFTNSVASYQCDNSDKEPPTYKPKGCPPLGDEGSTDLDYYPEEDT 300  
 Qy 301 EGDKVRPHTCPPCPAEPALGAPSVELPPPKPKDTLMSRTPETVTVVDSHEDPEYKFN 360  
 Db 301 EGDKVRPHTCPPCPAEPALGAPSVELPPPKPKDTLMSRTPETVTVVDSHEDPEYKFN 360  
 Qy 361 WYDGVEVHNAKTKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPVPPIEKTI 420  
 Db 361 WYDGVEVHNAKTKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPVPPIEKTI 420  
 Qy 421 SKAKGQPREPOVYTLPSREENTQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTP 480  
 Db 421 SKAKGQPREPOVYTLPSREENTQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTP 480  
 Qy 481 VLDSDGSFFFLYPSKLTVDKSRWQGNVFSCSVHEALINHYTOKSLSSLSPGK 531  
 Db 481 VLDSDGSFFFLYPSKLTVDKSRWQGNVFSCSVHEALINHYTOKSLSSLSPGK 531

RESULT 5  
 US-10-068-426-6  
 ; Sequence 6, Application US/10068426  
 ; Publication No. US003009157A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shaw, Gray D.  
 ; APPLICANT: Sako, Dianne S.  
 ; APPLICANT: Kumar, Ravindra  
 ; APPLICANT: Sullivan, Francis  
 ; APPLICANT: McDonagh, Tom  
 ; TITLE OF INVENTION: Platlet Glycoprotein IB Alpha Fusion Polypeptides and  
 ; FILE REFERENCE: 22058-503  
 ; CURRENT APPLICATION NUMBER: US/10/068,426  
 ; CURRENT FILING DATE: 2002-02-06  
 ; PRIORITY NUMBER: 60/266,838  
 ; PRIORITY FILING DATE: 2001-02-06  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SEQ ID NO 6  
 ; LENGTH: 531  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE: DOMAIN  
 ; NAME/KEY: DOMAIN  
 ; LOCATION: (1)-(531)  
 ; OTHER INFORMATION: GP1b290/1A-1G  
 ; US-10-068-426-6

Query Match 99.4%; Score 2823; DB 14; Length 531;  
 Best Local Similarity 99.4%; Pred. No. 1..2e-19;  
 Matches 528; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPPLLLPLPSLPHPHPICEVSKVASHLEVNCDKRNLTALEPDLPKDTTILHSENLY 60  
 Db 1 MPPLLLPLPSLPHPHPICEVSKVASHLEVNCDKRNLTALEPDLPKDTTILHSENLY 60  
 Qy 61 TFSLATLMPYTRUTQNLDRCELTKLQDGTLPVLTGLDSHNOQSPLLGOTLPALTV 120  
 Db 61 TFSLATLMPYTRUTQNLDRCELTKLQDGTLPVLTGLDSHNOQSPLLGOTLPALTV 120  
 Qy 121 LDYSFNRLTSLPLGALRGIGELOBLYLKGNEELKTLPPGILTPTPKLEKLSSLANNNLTELP 180  
 Db 121 LDYSFNRLTSLPLGALRGIGELOBLYLKGNEELKTLPPGILTPTPKLEKLSSLANNNLTELP 180

Query Match 99.6%; Score 2829; DB 15; Length 531;  
 Best Local Similarity 99.6%; Pred. No. 4..4e-200;  
 Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPPLLLPLPSLPHPHPICEVSKVASHLEVNCDKRNLTALEPDLPKDTTILHSENLY 60  
 Db 1 MPPLLLPLPSLPHPHPICEVSKVASHLEVNCDKRNLTALEPDLPKDTTILHSENLY 60  
 Qy 61 TFSLATLMPYTRUTQNLDRCELTKLQDGTLPVLTGLDSHNOQSPLLGOTLPALTV 120  
 Db 61 TFSLATLMPYTRUTQNLDRCELTKLQDGTLPVLTGLDSHNOQSPLLGOTLPALTV 120

|   |  |    |  |
|---|--|----|--|
| Qy  | 181 AGLLNGLENLDTLQLOENSLYTIPKOFFGSHLPPAFLHGNPWLNCCEILYFRWLQDNA 240   | Qy | 181 AGLLNGLENLDTLQLOENSLYTIPKOFFGSHLPPAFLHGNPWLNCCEILYFRWLQDNA 240   |
| Db  | 181 AGLLNGLENLDTLQLOENSLYTIPKOFFGSHLPPAFLHGNPWLNCCEILYFRWLQDNA 240   | Db | 181 AGLLNGLENLDTLQLOENSLYTIPKOFFGSHLPPAFLHGNPWLNCCEILYFRWLQDNA 240   |
| Qy  | 241 ENVYWKQVYDVKAVTSVNAVASQCDNSDKFPPVVKYFGKGCPFTLGDGDTPDLYYPEEDE 300 | Qy | 241 ENVYWKQVYDVKAVTSVNAVASQCDNSDKFPPVVKYFGKGCPFTLGDGDTPDLYYPEEDE 300 |
| Db  | 241 ENVYWKQGVDAAMTSVNAVASQCDNSDKFPPVVKYFGKGCPFTLGDGDTPDLYYPEEDE 300  | Db | 241 ENVYWKQVYDVKAVTSVNAVASQCDNSDKFPPVVKYFGKGCPFTLGDGDTPDLYYPEEDE 300 |
| Qy  | 301 EGDKVPRHTCPCPAFLGAPSFLFPKPKDFTLMSRPEVTCVYVYDHSHEPEVKEN 360       | Qy | 301 EGDKVPRHTCPCPAFLGAPSFLFPKPKDFTLMSRPEVTCVYVYDHSHEPEVKEN 360       |
| Db  | 301 EGDKVPRHTCPCPAFLGAPSFLFPKPKDFTLMSRPEVTCVYVYDHSHEPEVKEN 360       | Db | 301 EGDKVPRHTCPCPAFLGAPSFLFPKPKDFTLMSRPEVTCVYVYDHSHEPEVKEN 360       |
| Qy  | 361 WYDGVEVHNAKTKEPEQVNSTYRVSVLHQDWLNGKEYKCVSNKALPVPIEKT 420         | Qy | 361 WYDGVEVHNAKTKEPEQVNSTYRVSVLHQDWLNGKEYKCVSNKALPVPIEKT 420         |
| Db  | 361 WYDGVEVHNAKTKEPEQVNSTYRVSVLHQDWLNGKEYKCVSNKALPVPIEKT 420         | Db | 361 WYDGVEVHNAKTKEPEQVNSTYRVSVLHQDWLNGKEYKCVSNKALPVPIEKT 420         |
| Qy  | 421 SKAKGQPREPVQYTLPPSREEMTKQVSLLTCLVKGFPYPSDIAVEMSGOPENNYKTPP 480   | Qy | 421 SKAKGQPREPVQYTLPPSREEMTKQVSLLTCLVKGFPYPSDIAVEMSGOPENNYKTPP 480   |
| Db  | 421 SKAKGQPREPVQYTLPPSREEMTKQVSLLTCLVKGFPYPSDIAVEMSGOPENNYKTPP 480   | Db | 421 SKAKGQPREPVQYTLPPSREEMTKQVSLLTCLVKGFPYPSDIAVEMSGOPENNYKTPP 480   |
| Qy  | 481 VLDSGSSFFFLYSLKLTVDKSRWQOQNRVFSCSVMEHALHNHYTQKSLSLSPGK 531       | Qy | 481 VLDSGSSFFFLYSLKLTVDKSRWQOQNRVFSCSVMEHALHNHYTQKSLSLSPGK 531       |
| Db  | 481 VLDSGSSFFFLYSLKLTVDKSRWQOQNRVFSCSVMEHALHNHYTQKSLSLSPGK 531       | Db | 481 VLDSGSSFFFLYSLKLTVDKSRWQOQNRVFSCSVMEHALHNHYTQKSLSLSPGK 531       |
| RESULT 7  |  |    |  |
| US-10-068-426-3   |  |    |  |
| ; Sequence 3, Application US/10008426   |  |    |  |
| ; Publication No. US20030091576A1   |  |    |  |
| ; GENERAL INFORMATION:  |  |    |  |
| ; APPLICANT: Shaw, Gray D.  |  |    |  |
| ; APPLICANT: Sako, Dianne S.  |  |    |  |
| ; APPLICANT: Sullivan, Francis  |  |    |  |
| ; APPLICANT: McDonagh, Tom  |  |    |  |
| ; TITLE OF INVENTION: Platlet Glycoprotein IB Alpha Fusion Polypeptides and                         |  |    |  |
| ; TITLE OF INVENTION: Platlet Glycoprotein IB Alpha Fusion Polypeptides and Methods of Use Thereof  |  |    |  |
| ; FILE REFERENCE: 22058-503   |  |    |  |
| ; CURRENT APPLICATION NUMBER: US/10/382,758   |  |    |  |
| ; CURRENT FILING DATE: 2003-03-06   |  |    |  |
| ; PRIOR APPLICATION NUMBER: US/10/068,426   |  |    |  |
| ; PRIOR FILING DATE: 2002-02-06   |  |    |  |
| ; PRIOR APPLICATION NUMBER: 6,0/266,838   |  |    |  |
| ; PRIOR FILING DATE: 2001-02-06   |  |    |  |
| ; NUMBER OF SEQ ID NOS: 20  |  |    |  |
| ; SOFTWARE: PatentIn Ver. 2.1   |  |    |  |
| ; SEQ ID NO 6   |  |    |  |
| ; LENGTH: 531   |  |    |  |
| ; TYPE: PRT   |  |    |  |
| ; ORGANISM: Homo sapiens  |  |    |  |
| ; FEATURE: DOMAIN   |  |    |  |
| ; NAME/KEY: DOMAIN  |  |    |  |
| ; LOCATION: (1)..(531)  |  |    |  |
| ; OTHER INFORMATION: GP1b302/4K-1G  |  |    |  |
| US-10-068-426-3   |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| US-10-068-758-6   |  |    |  |
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| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local Similarity 99.4%; Pred. No. 1.4e-199; Matches 528; Conservative 1; Mismatches 0; Gaps 0; |  |    |  |
| ; Other Information: GP1b290/1A-1g  |  |    |  |
| Query Match 99.4%; Score 2823; DB 15; Length 531;   |  |    |  |
| Best Local  |  |    |  |

Qy 241 ENTYWVKQVVDYKAVTSNTAVSQCDNSDKFPIVYKYPGKCPPIGDEGPTDLYDYPEEDT 300  
 Db 241 ENTYWVKQVVDYKAVTSNTAVSQCDNSDKFPIVYKYPGKCPPIGDEGPTDLYDYPEEDT 300  
 Qy 301 EGDKV-----RPHTCPPCPAPEALGAPSVELFPKPKDTLMISRTPEVTCV 347  
 Db 301 EGDKVAATATVVKPPTKARPHTCPPCPAPEALGAPSVELFPKPKDTLMISRTPEVTCV 360  
 Qy 348 VDISHEDPPIVKEWYVDGVEVNAKTKPREEQNSTRVSVTLYHQDWLNGKEYCKV 407  
 Db 361 VDISHEDPPIVKEWYVDGVEVNAKTKPREEQNSTRVSVTLYHQDWLNGKEYCKV 420  
 Qy 408 SNKALPVPIEKTISKAQGPREQQVYTLPSREEMTKNQVSLSCLVKGFPSPDIAVEWS 467  
 Db 421 SNKALPVPIEKTISKAQGPREQQVYTLPSREEMTKNQVSLSCLVKGFPSPDIAVEWS 480  
 Qy 468 NGQPENNYKTTPPVLDSDGSFLYSLKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSL 527  
 Db 481 NGQPENNYKTTPPVLDSDGSFLYSLKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSL 540  
 Qy 528 SPGK 531  
 Db 541 SPGK 544

Qy 528 SPGK 531  
 Db 541 SPGK 544

RESULT 8  
 US-10-382-758-3  
 Sequence 3, Application US/10382758  
 Publication No. US20030232047A1  
 GENERAL INFORMATION:  
 APPLICANT: Shaw, Gray D.  
 APPLICANT: Sako, Dianne S.  
 APPLICANT: Kumar, Ravindra  
 APPLICANT: Sullivan, Francis  
 APPLICANT: McDonagh, Tom  
 TITLE OF INVENTION: Platlet Glycoprotein IB Alpha Fusion Polypeptides and Methods of Use Thereof  
 FILE REFERENCE: 22058-503  
 CURRENT APPLICATION NUMBER: US/10/382,758  
 CURRENT FILING DATE: 2003-03-06  
 PRIOR APPLICATION NUMBER: US/10/068,426  
 PRIOR FILING DATE: 2002-02-06  
 PRIOR APPLICATION NUMBER: 60/266,838  
 PRIOR FILING DATE: 2001-02-06  
 NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 544  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: DOMAIN  
 NAME/KEY: DOMAIN  
 LOCATION: (1) . . . (544)  
 OTHER INFORMATION: GPLb302/4X-1g  
 US-10-382-758-3

Query Match 99.4%; Score 2822.5; DB 15; Length 544;  
 Best Local Similarity 97.6%; Pred. No. 1..e-199;  
 Matches 531; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 MPLILLILLPSLPHPHPICEVSKVASHLEVNCDKRNITALPDDLPKDTTILHSENLLY 60  
 Db 1 MPLILLILLPSLPHPHPICEVSKVASHLEVNCDKRNITALPDDLPKDTTILHSENLLY 60  
 Qy 61 TFSLATIMPYTRTQLNLDRCLETKLQVDTGLPVLGTLDSHLNQLQSLPLLGOTLPALTV 120  
 Db 61 TFSLATIMPYTRTQLNLDRCLETKLQVDTGLPVLGTLDSHLNQLQSLPLLGOTLPALTV 120  
 Qy 121 LDVSFNRLTSLPLGALRGEQELYLGNEKLTKLPPGILTPTPKLEKLSSLANNNLTEP 180  
 Db 121 LDVSFNRLTSLPLGALRGEQELYLGNEKLTKLPPGILTPTPKLEKLSSLANNNLTEP 180

Qy 181 AGILNGLENLDTLLQENSLSYTIPKGFFGSHLUPPAFHGNPWLNCBILYPRRMQDNA 240  
 Db 181 AGILNGLENLDTLLQENSLSYTIPKGFFGSHLUPPAFHGNPWLNCBILYPRRMQDNA 240  
 Qy 241 ENTYWVKQVVDYKAVTSNTAVSQCDNSDKFPIVYKYPGKCPPIGDEGPTDLYDYPEEDT 300  
 Db 241 ENTYWVKQVVDYKAVTSNTAVSQCDNSDKFPIVYKYPGKCPPIGDEGPTDLYDYPEEDT 300  
 Qy 301 EGDKV-----RPHTCPPCPAPEALGAPSVELFPKPKDTLMISRTPEVTCV 347  
 Db 301 EGDKV-----RPHTCPPCPAPEALGAPSVELFPKPKDTLMISRTPEVTCV 360  
 Qy 348 VDISHEDPPIVKEWYVDGVEVNAKTKPREEQNSTRVSVTLYHQDWLNGKEYCKV 407  
 Db 361 VDISHEDPPIVKEWYVDGVEVNAKTKPREEQNSTRVSVTLYHQDWLNGKEYCKV 420  
 Qy 348 VDISHEDPPIVKEWYVDGVEVNAKTKPREEQNSTRVSVTLYHQDWLNGKEYCKV 407  
 Db 361 VDISHEDPPIVKEWYVDGVEVNAKTKPREEQNSTRVSVTLYHQDWLNGKEYCKV 420  
 Qy 408 SNKALPVPIEKTISKAQGPREQQVYTLPSREEMTKNQVSLSCLVKGFPSPDIAVEWS 467  
 Db 421 SNKALPVPIEKTISKAQGPREQQVYTLPSREEMTKNQVSLSCLVKGFPSPDIAVEWS 480  
 Qy 468 NGQPENNYKTTPPVLDSDGSFLYSLKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSL 527  
 Db 481 NGQPENNYKTTPPVLDSDGSFLYSLKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSL 540  
 Qy 528 SPGK 531  
 Db 541 SPGK 544

RESULT 9  
 US-10-068-426-1  
 Sequence 1, Application US/10068426  
 Publication No. US2003009157A1  
 GENERAL INFORMATION:  
 APPLICANT: Shaw, Gray D.  
 APPLICANT: Sako, Dianne S.  
 APPLICANT: Kumar, Ravindra  
 APPLICANT: Sullivan, Francis  
 APPLICANT: McDonagh, Tom  
 TITLE OF INVENTION: Platlet Glycoprotein IB Alpha Fusion Polypeptides and Methods of Use Thereof  
 FILE REFERENCE: 22058-503  
 CURRENT APPLICATION NUMBER: US/10/068,426  
 CURRENT FILING DATE: 2002-02-06  
 PRIORITY APPLICATION NUMBER: 60/266,838  
 PRIORITY FILING DATE: 2001-02-06  
 NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 544  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (1) . . . (544)  
 OTHER INFORMATION: GPLb302-1g  
 US-10-068-426-1

Query Match 99.1%; Score 2812.5; DB 14; Length 544;  
 Best Local Similarity 97.2%; Pred. No. 7..4e-199;  
 Matches 529; Conservative 1; Mismatches 1; Indels 13; Gaps 1;

Qy 1 MPLLILLILLPSLPHPHPICEVSKVASHLEVNCDKRNITALPDDLPKDTTILHSENLLY 60  
 Db 1 MPLLILLILLPSLPHPHPICEVSKVASHLEVNCDKRNITALPDDLPKDTTILHSENLLY 60  
 Qy 61 TFSLATIMPYTRTQLNLDRCLETKLQVDTGLPVLGTLDSHLNQLQSLPLLGOTLPALTV 120  
 Db 61 TFSLATIMPYTRTQLNLDRCLETKLQVDTGLPVLGTLDSHLNQLQSLPLLGOTLPALTV 120  
 Qy 121 LDVSFNRLTSLPLGALRGEQELYLGNEKLTKLPPGILTPTPKLEKLSSLANNNLTEP 180  
 Db 121 LDVSFNRLTSLPLGALRGEQELYLGNEKLTKLPPGILTPTPKLEKLSSLANNNLTEP 180

|                 |   |  |     |                 |   |  |     |
|-----------------|---|--|-----|-----------------|---|--|-----|
| Qy              | 181   | AGLNLGLENLDTLQENSILTYIPIKOFFGSHLPPAFLHNPNWLNCETILYFRRLQDNA     | 240 | Db              | 121   | LDVSPNRLTSLPLGALRGGLQELYLGNGNLKTKTIPPGLLTPTPKLEKLSANNLTEL      | 180 |
| Db              | 181   | AGLNLGLENLDTLQENSILTYIPIKOFFGSHLPPAFLHNPNWLNCETILYFRRLQDNA     | 240 | Qy              | 181   | AGLNLGLENLDTLQENSILTYIPIKOFFGSHLPPAFLHNPNWLNCETILYFRRLQDNA     | 240 |
| Qy              | 241   | ENVYWKQVVDVKAVTSVNASVQCONSDFKDPVYKPGKGCPTLGDEGDTDLIDYYPEEDT    | 300 | Db              | 181   | AGLNLGLENLDTLQENSILTYIPIKOFFGSHLPPAFLHNPNWLNCETILYFRRLQDNA     | 240 |
| Db              | 241   | ENVYWKQVVDVKAVTSVNASVQCONSDFKDPVYKPGKGCPTLGDEGDTDLIDYYPEEDT    | 300 | Qy              | 241   | ENVYWKQVVDVKAVTSVNASVQCONSDFKDPVYKPGKGCPTLGDEGDTDLIDYYPEEDT    | 300 |
| Qy              | 301   | EGDKV-----RPHTCPPAPEALGASVFLPPKPKDTLMSRTPVEPTCVV               | 347 | Db              | 241   | ENVYWKQVVDVKAVTSVNASVQCONSDFKDPVYKPGKGCPTLGDEGDTDLIDYYPEEDT    | 300 |
| Db              | 301   | EGDKV-----RPHTCPPAPEALGASVFLPPKPKDTLMSRTPVEPTCVV               | 347 | Qy              | 301   | EGDKV-----RPHTCPPAPEALGASVFLPPKPKDTLMSRTPVEPTCVV               | 347 |
| Db              | 301   | EGDKV-----RPHTCPPAPEALGASVFLPPKPKDTLMSRTPVEPTCVV               | 360 | Db              | 301   | EGDKV-----RPHTCPPAPEALGASVFLPPKPKDTLMSRTPVEPTCVV               | 360 |
| Qy              | 348   | VDVSHEDPEYKFNWYDGVYEVHNAKTKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKV     | 407 | Qy              | 348   | VDVSHEDPEYKFNWYDGVYEVHNAKTKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKV     | 407 |
| Db              | 361   | VDVSHEDPEYKFNWYDGVYEVHNAKTKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKV     | 420 | Db              | 361   | VDVSHEDPEYKFNWYDGVYEVHNAKTKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKV     | 420 |
| Qy              | 408   | SNKALPVPIEKTISAKGQPREPOQYTLPPSREENTKNOVSLTCLVKGKPSDIAVWES      | 467 | Qy              | 408   | SNKALPVPIEKTISAKGQPREPOQYTLPPSREENTKNOVSLTCLVKGKPSDIAVWES      | 467 |
| Db              | 421   | SNKALPVPIEKTISAKGQPREPOQYTLPPSREENTKNOVSLTCLVKGKPSDIAVWES      | 480 | Db              | 421   | SNKALPVPIEKTISAKGQPREPOQYTLPPSREENTKNOVSLTCLVKGKPSDIAVWES      | 480 |
| Qy              | 468   | NGQPENNYKTTAPPVLDGSFFFLYSLTVLDSKSRWQOGNVSFCSVNHAEALHNHYTOKSLSL | 527 | Qy              | 468   | NGQPENNYKTTAPPVLDGSFFFLYSLTVLDSKSRWQOGNVSFCSVNHAEALHNHYTOKSLSL | 527 |
| Db              | 481   | NGQPENNYKTTAPPVLDGSFFFLYSLTVLDSKSRWQOGNVSFCSVNHAEALHNHYTOKSLSL | 540 | Db              | 481   | NGQPENNYKTTAPPVLDGSFFFLYSLTVLDSKSRWQOGNVSFCSVNHAEALHNHYTOKSLSL | 540 |
| Qy              | 528   | SPGK 531   |     | Qy              | 528   | SPGK 531   |     |
| Db              | 541   | SPGK 544   |     | Db              | 541   | SPGK 544   |     |
| RESULT 10       |   |  |     |                 |   |  |     |
| US-10-068-426-2 |   |  |     | US-10-068-426-2 |   |  |     |
| ;               | Sequence 1, Application US/10068426   |  |     | ;               | Sequence 1, Application US/10068426   |  |     |
| ;               | Publication No. US20030091576A1   |  |     | ;               | Publication No. US20030091576A1   |  |     |
| ;               | GENERAL INFORMATION:  |  |     | ;               | GENERAL INFORMATION:  |  |     |
| ;               | APPLICANT: Shaw, Gray D.  |  |     | ;               | APPLICANT: Shaw, Gray D.  |  |     |
| ;               | APPLICANT: Sako, Dianne S.  |  |     | ;               | APPLICANT: Sako, Dianne S.  |  |     |
| ;               | APPLICANT: Kumar, Ravindra  |  |     | ;               | APPLICANT: Kumar, Ravindra  |  |     |
| ;               | APPLICANT: Sullivan, Francis  |  |     | ;               | APPLICANT: Sullivan, Francis  |  |     |
| ;               | APPLICANT: McDonagh, Tom  |  |     | ;               | APPLICANT: McDonagh, Tom  |  |     |
| ;               | TITLE OF INVENTION: Platlet Glycoprotein IB Alpha Fusion Polypeptides and                   |  |     | ;               | TITLE OF INVENTION: Platlet Glycoprotein IB Alpha Fusion Polypeptides and                   |  |     |
| ;               | FILE REFERENCE: 22058-503   |  |     | ;               | FILE REFERENCE: 22058-503   |  |     |
| ;               | CURRENT APPLICATION NUMBER: US/10/068,426   |  |     | ;               | CURRENT APPLICATION NUMBER: US/10/302,758   |  |     |
| ;               | CURRENT FILING DATE: 2002-02-06   |  |     | ;               | CURRENT FILING DATE: 2003-03-06   |  |     |
| ;               | PRIOR APPLICATION NUMBER: 60/266,838  |  |     | ;               | PRIOR APPLICATION NUMBER: US/10/068,426   |  |     |
| ;               | PRIOR FILING DATE: 2001-02-06   |  |     | ;               | PRIOR FILING DATE: 2001-02-06   |  |     |
| ;               | NUMBER OF SEQ ID NOS: 20  |  |     | ;               | PRIOR APPLICATION NUMBER: 60/266,838  |  |     |
| ;               | SOFTWARE: PatentIn Ver. 2.1   |  |     | ;               | PRIOR FILING DATE: 2001-02-06   |  |     |
| ;               | SEQ ID NO 2   |  |     | ;               | NUMBER OF SEQ ID NOS: 20  |  |     |
| ;               | LENGTH: 544   |  |     | ;               | SOFTWARE: PatentIn Ver. 2.1   |  |     |
| ;               | TYPE: PRT   |  |     | ;               | SEQ ID NO 1   |  |     |
| ;               | ORGANISM: Homo sapiens  |  |     | ;               | LENGTH: 544   |  |     |
| ;               | FEATURE: DOMAIN   |  |     | ;               | TYPE: PRT   |  |     |
| ;               | NAME/KEY: DOMAIN  |  |     | ;               | ORGANISM: Homo sapiens  |  |     |
| ;               | LOCATION: (1) .. (544)  |  |     | ;               | FEATURE:  |  |     |
| ;               | OTHER INFORMATION: GP1b302/2A-19  |  |     | ;               | NAME/KEY: DOMAIN  |  |     |
| ;               | US-10-068-426-2   |  |     | ;               | LOCATION: (1) .. (544)  |  |     |
| ;               | Query Match 99.1%; Score 2812.5; DB 14; Length 544;   |  |     | ;               | OTHER INFORMATION: GP1b302-19   |  |     |
| ;               | Best Local Similarity 97.2%; Pred. No. 7.4e-199; Matches 529; Conservative 1; Mismatches 1; |  |     | ;               | US-10-382-758-1   |  |     |
| ;               | Query Match 99.1%; Score 2812.5; DB 15; Length 544;   |  |     | ;               | Query Match 99.1%; Score 2812.5; DB 15; Length 544;   |  |     |
| ;               | Best Local Similarity 97.2%; Pred. No. 7.4e-199; Matches 529; Conservative 1; Mismatches 1; |  |     | ;               | Best Local Similarity 97.2%; Pred. No. 7.4e-199; Matches 529; Conservative 1; Mismatches 1; |  |     |
| ;               | Query Match 99.1%; Score 2812.5; DB 15; Length 544;   |  |     | ;               | Query Match 99.1%; Score 2812.5; DB 15; Length 544;   |  |     |
| ;               | ;   |  |     | ;               | ;   |  |     |
| Qy              | 1   | MPLLLLLLPSLPHPHPICEVKASHLBNCDKRNLTAIPDLPKDTTLHLSENLLY          | 60  | Qy              | 1   | MPLLLLLLPSLPHPHPICEVKASHLBNCDKRNLTAIPDLPKDTTLHLSENLLY          | 60  |
| Db              | 1   | MPLLLLLLPSLPHPHPICEVKASHLBNCDKRNLTAIPDLPKDTTLHLSENLLY          | 60  | Db              | 1   | MPLLLLLLPSLPHPHPICEVKASHLBNCDKRNLTAIPDLPKDTTLHLSENLLY          | 60  |
| Qy              | 61  | TFSLATLMPYTRITQLNLDCELTKLQVQDTLPIVGLTLDLISHNQQLQSLPLGQTLPA     | 120 | Qy              | 61  | TFSLATLMPYTRITQLNLDCELTKLQVQDTLPIVGLTLDLISHNQQLQSLPLGQTLPA     | 120 |
| Db              | 61  | TFSLATLMPYTRITQLNLDCELTKLQVQDTLPIVGLTLDLISHNQQLQSLPLGQTLPA     | 120 | Db              | 61  | TFSLATLMPYTRITQLNLDCELTKLQVQDTLPIVGLTLDLISHNQQLQSLPLGQTLPA     | 120 |
| Qy              | 121   | LDVSPNRLTSLPLGALRGGLQELYLGNGNLKTKTIPPGLLTPTPKLEKLSANNLTEL      | 180 | Qy              | 121   | LDVSPNRLTSLPLGALRGGLQELYLGNGNLKTKTIPPGLLTPTPKLEKLSANNLTEL      | 180 |

Qy 121 LDYSFNRLTSLPLGALRGIGELQEIYIKKNEELKTLPPGLLTPPRPKLEKISLANNNLTELP 180  
 Db 121 LDYSFNRLTSLPLGALRGIGELQEIYIKKNEELKTLPPGLLTPPRPKLEKISLANNNLTELP 180  
 Qy 181 AGLINGLENLDTLQLQNSLYTPKGFPGSHLPPAFIQLGNPMLCNCBILYPRWLQDNA 240  
 Db 181 AGLINGLENLDTLQLQNSLYTPKGFPGSHLPPAFIQLGNPMLCNCBILYPRWLQDNA 240  
 Qy 241 ENYVWIKQVQVYDVKATSNAVASQCDNSKDFPKVYKPGKCPGTLGDEGTDLYDYPEEDT 300  
 Db 241 ENYVWIKQVQVYDVKATSNAVASQCDNSKDFPKVYKPGKCPGTLGDEGTDLYDYPEEDT 300  
 Qy 301 EGDKV------RPHTCPPCPAPEALGAPSVPFLPPKPKD7LIM1SRTPE7TCV 347  
 Db 301 EGDKV------RPHTCPPCPAPEALGAPSVPFLPPKPKD7LIM1SRTPE7TCV 360  
 Qy 348 VDVSHEDPPEVKPFWYDGVEVNAKTRKEEQYNSTTRVSVLTVLHQDWLNGKEYKCKV 407  
 Db 361 VDVSHEDPPEVKPFWYDGVEVNAKTRKEEQYNSTTRVSVLTVLHQDWLNGKEYKCKV 420  
 Qy 408 SNKALPVPEPEKTISSKAKCPREPVYTLPPSR8EMTKNQVSUTCLVKGCPYPSDIAVEWES 467  
 Db 421 SNKALPVPEPEKTISSKAKCPREPVYTLPPSR8EMTKNQVSUTCLVKGCPYPSDIAVEWES 480  
 Qy 468 NGQPENNYKTTPPVLDSDCSFPLYSKLTVDKSRWQGNTVFSCSVMHEALHNHYTQKSLSL 527  
 Db 481 NGQPENNYKTTPPVLDSDCSFPLYSKLTVDKSRWQGNTVFSCSVMHEALHNHYTQKSLSL 540  
 Qy 528 SPGK 531  
 Db 541 SPGK 544

Qy 541 SPGK 544

Db 541 SPGK 544

RESULT 12  
 US-10-382-758-2  
 ; Sequence 2, Application US/10182758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shaw, Gray D.  
 ; APPLICANT: Sako, Diane S.  
 ; APPLICANT: Kumar, Ravindra  
 ; APPLICANT: Sullivan, Francis  
 ; APPLICANT: McDonald, Tom  
 ; TITLE OF INVENTION: Platlet Glycoprotein IB Alpha Fusion Polypeptides and  
 ; FILE REFERENCE: 22058-503  
 ; CURRENT APPLICATION NUMBER: US/10/382,758  
 ; PRIOR APPLICATION NUMBER: US/10/068,426  
 ; PRIOR FILING DATE: 2002-02-06  
 ; PRIOR APPLICATION NUMBER: 60/266,838  
 ; PRIOR FILING DATE: 2001-02-06  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 2  
 ; LENGTH: 544  
 ; TYPE: PPT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE: DOMAIN  
 ; NAME/KEY: DOMAIN  
 ; OTHER INFORMATION: GP1b302/2A-1g

US-10-382-758-2

Query Match 99.1%; Score 2812.5; DB 15; Length 544; i:\*,? ;  
 Best Local Similarity 97.2%; Prd. No. 7.4e-199; 1; Mismatches 1; Indels 13; Gaps 1;

Qy 1 MPPLLLPLSPHPPCIEVSKVASHLEVNCDKRNLTALEPDLPKDTTILHSENLY 60  
 Db 1 MPPLLLPLSPHPPCIEVSKVASHLEVNCDKRNLTALEPDLPKDTTILHSENLY 60

Qy 61 TFSLATLMPYTRLTQNLIDRCBLTQLQYDGTLPVLTQNLQSPPLGOTLPALTV 120  
 Db 61 TFSLATLMPYTRLTQNLIDRCBLTQLQYDGTLPVLTQNLQSPPLGOTLPALTV 120

Qy 61 TFSLATLMPYTRLTQNLIDRCBLTQLQYDGTLPVLTQNLQSPPLGOTLPALTV 120  
 Db 61 TFSLATLMPYTRLTQNLIDRCBLTQLQYDGTLPVLTQNLQSPPLGOTLPALTV 120

RESULT 13  
 US-10-408-765A-430  
 ; Sequence 430, Application US/10408765A  
 ; Publication No. US20040101874A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Fahy, Eoin D.  
 ; APPLICANT: Zhang, Bing  
 ; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Taylor, Steven W.  
 ; APPLICANT: Glenn, Gary M.  
 ; APPLICANT: Warnock, Dale E.  
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 ; FILE REFERENCE: 656088 465  
 ; CURRENT APPLICATION NUMBER: US/10/408,765A  
 ; NUMBER OF SEQ ID NOS: 3077  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 430  
 ; LENGTH: 626  
 ; TYPE: PPT  
 ; ORGANISM: Homo sapiens  
 ; US-10-408-765A-430

Query Match 56.9%; Score 1615.5; DB 16; Length 626;  
 Best Local Similarity 84.2%; Prd. No. 1.7e-110; 5; Mismatches 20; Indels 35; Gaps 5;

Qy 121 LDVSFNRLLTSLPLGAIRGLGEQELYLKGNELKTLDPGLLTPTPKLEKLSIANNNLTELP 180  
 Db 121 LDVSFNRLLTSLPLGAIRGLGEQELYLKGNELKTLDPGLLTPTPKLEKLSIANNNLTELP 180  
 Qy 181 AGLLNGLENLDTLLOENSLYTIKPSFFGSHLPPAFLHNPNWLNCCEILYFRRWLQDNA 240  
 Db 181 AGLLNGLENLDTLLOENSLYTIKPSFFGSHLPPAFLHNPNWLNCCEILYFRRWLQDNA 240  
 Qy 241 ENVYWKQKQVVDYKAVTSNVAQCDNSDKFVVKYKPGKGCPTLGEGDTDLYDYPEEDT 300  
 Db 241 ENVYWKQKQVVDYKAVTSNVAQCDNSDKFVVKYKPGKGCPTLGEGDTDLYDYPEEDT 300  
 Qy 301 EGDVKR-----PHTCP-----PCPA---PEALGAPSVELFPKK-- 330  
 Db 301 EGDVKR-----PHTCP-----PCPA---PEALGAPSVELFPKK-- 330  
 Qy 331 PKDTL---MISRTPEVT 344  
 Db 361 PNFTLAMESETFSKTPKST 379  
 Qy 331 PKDTL---MISRTPEVT 344  
 Db 361 PNFTLAMESETFSKTPKST 379

RESULT 14  
 US-10-741-600-1496  
 ; Sequence 1496, Application US/10741600  
 ; Publication No. US200500261620A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: C10/01499  
 ; CURRENT FILING DATE: 2003-12-22  
 ; NUMBER OF SEQ ID NOS: 73997  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 1496  
 ; LENGTH: 626  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FILE REFERENCE: US/10/741,600  
 ; CURRENT FILING DATE: 2003-12-22  
 ; NUMBER OF SEQ ID NOS: 73997  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 1496  
 ; LENGTH: 626  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-741-600-1496

Query Match, Best Local Similarity 56.9%, Score 1615.5, DB 17, Length 626;  
 Matches 319; Conservative 5; Missmatches 20; Indels 35; Gaps 5;

Qy 1 MPLLILLLSPHLPHPICSVKASHLEYNCRNLTAIPDLPKDTTLIHLSENLY 60  
 Db 1 MPLLILLLSPHLPHPICSVKASHLEYNCRNLTAIPDLPKDTTLIHLSENLY 60  
 Qy 61 TFSLATLMPYTRLTLQNLDRSELTKLQVDTLPVLTLDISHNQLQSLPLIGOTLPALTY 120  
 Db 61 TFSLATLMPYTRLTLQNLDRSELTKLQVDTLPVLTLDISHNQLQSLPLIGOTLPALTY 120  
 Qy 121 LDVSFNRLLTSLPLGAIRGLGEQELYLKGNELKTLDPGLLTPTPKLEKLSIANNNLTELP 180  
 Db 121 LDVSFNRLLTSLPLGAIRGLGEQELYLKGNELKTLDPGLLTPTPKLEKLSIANNNLTELP 180

Qy 181 AGLLNGLENLDTLLOENSLYTIKPSFFGSHLPPAFLHNPNWLNCCEILYFRRWLQDNA 240  
 Db 181 AGLLNGLENLDTLLOENSLYTIKPSFFGSHLPPAFLHNPNWLNCCEILYFRRWLQDNA 240  
 Qy 241 ENVYWKQKQVVDYKAVTSNVAQCDNSDKFVVKYKPGKGCPTLGEGDTDLYDYPEEDT 300  
 Db 241 ENVYWKQKQVVDYKAVTSNVAQCDNSDKFVVKYKPGKGCPTLGEGDTDLYDYPEEDT 300  
 Qy 301 EGDVKR-----PHTCP-----PCPA---PEALGAPSVELFPKK-- 330  
 Db 301 EGDVKR-----PHTCP-----PCPA---PEALGAPSVELFPKK-- 330  
 Qy 331 PKDTL---MISRTPEVT 344  
 Db 361 PNFTLAMESETFSKTPKST 379

Query Match, Best Local Similarity 100.0%, Score 1536, DB 14, Length 290;  
 Matches 290; Conservative 0; Missmatches 0; Indels 0; Gaps 0;  
 Db 17 HPICVSKVASHLEYNCRNLTAIPDLPKDTTLIHLSENLYTFSLATLMPYTRLTLQ 76  
 Db 1 HPICVSKVASHLEYNCRNLTAIPDLPKDTTLIHLSENLYTFSLATLMPYTRLTLQ 60  
 Qy 77 NLDRCEBLTQLQVDTLPVLTLDISHNQLQSLPLIGOTLPALTYDVSFNRLTSLPLGAL 136  
 Db 61 NLDRCEBLTQLQVDTLPVLTLDISHNQLQSLPLIGOTLPALTYDVSFNRLTSLPLGAL 120  
 Qy 137 RGLGEHQELYLGKGNLKTLPGLLTPTPKLEKLSIANNNLTELPAGLNGLENLTLLQ 196  
 Db 121 RGLGEHQELYLGKGNLKTLPGLLTPTPKLEKLSIANNNLTELPAGLNGLENLTLLQ 180  
 Qy 197 ENSLYTIPKQFFGSHLPPAFLHNPNWLNCCEILYFRRWLQDNAENVYWKQVVDVKAVT 256  
 Db 181 ENSLYTIPKQFFGSHLPPAFLHNPNWLNCCEILYFRRWLQDNAENVYWKQVVDVKAVT 240  
 Qy 257 SNAVSVQCDNSDKFVVKYKPGKGCPTLGEGDTDLYDYPEEDTGDVKR 306  
 Db 241 SNAVSVQCDNSDKFVVKYKPGKGCPTLGEGDTDLYDYPEEDTGDVKR 290

Search completed: May 24, 2005, 06:16:23  
 Job time : 138 secs

GenCore version 5.1.6  
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## Om protein - protein search, using sw model

Run on: May 24, 2005, 05:54:11 ; Search time 42 Seconds

(without alignments)  
 943.777 Million cell updates/sec

Title: US-10-068-426-5

Perfect score: 2839

Sequence: 1 MPLLLLLLPSLPHPHIC.....MHEALHNHYTQKSLSLSPGK 531

Scoring table: BLOSUM62

Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Issued\_Patents\_AA:\*

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1: /cgn2_6/ptodata/1/iaa/5A_COMBO.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMBO.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMBO.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMBO.pep:*
5: /cgn2_6/ptodata/1/iaa/PCNTS_COMBO.pep:*
6: /cgn2_6/ptodata/1/iaa/backtles1.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID               | Description        |
|------------|--------|-------------|--------|---------------------|--------------------|
| 1          | 1528.5 | 53.8        | 320    | 1 US-07-613-083B-1  | Sequence 1, Appli  |
| 2          | 1521.5 | 53.6        | 610    | 1 US-07-821-717B-6  | Sequence 6, Appli  |
| 3          | 1521.5 | 53.6        | 610    | 1 US-08-119-262B-11 | Sequence 6, Appli  |
| 4          | 1521.5 | 53.6        | 610    | 1 US-08-135-929A-11 | Sequence 11, Appli |
| 5          | 1521.5 | 53.6        | 610    | 1 US-08-234-265A-11 | Sequence 11, Appli |
| 6          | 1237   | 43.6        | 313    | 3 US-08-713-555B-36 | Sequence 36, Appli |
| 7          | 1230   | 43.3        | 388    | 3 US-09-131-247-16  | Sequence 16, Appli |
| 8          | 1230   | 43.3        | 388    | 4 US-09-784-623-16  | Sequence 16, Appli |
| 9          | 1230   | 43.3        | 449    | 3 US-08-897-236-23  | Sequence 23, Appli |
| 10         | 1230   | 43.3        | 449    | 4 US-09-500-253B-23 | Sequence 23, Appli |
| 11         | 1226.5 | 43.2        | 397    | 4 US-08-775-066-2   | Sequence 2, Appli  |
| 12         | 1223   | 43.1        | 451    | 2 US-08-887-352B-14 | Sequence 14, Appli |
| 13         | 1223   | 43.1        | 451    | 2 US-08-887-352B-18 | Sequence 16, Appli |
| 14         | 1223   | 43.1        | 451    | 2 US-08-887-352B-18 | Sequence 18, Appli |
| 15         | 1223   | 43.1        | 451    | 3 US-08-466-151-65  | Sequence 65, Appli |
| 16         | 1223   | 43.1        | 451    | 3 US-09-109-207C-14 | Sequence 14, Appli |
| 17         | 1223   | 43.1        | 451    | 3 US-09-109-207C-14 | Sequence 16, Appli |
| 18         | 1223   | 43.1        | 451    | 3 US-09-109-207C-18 | Sequence 18, Appli |
| 19         | 1223   | 43.1        | 451    | 3 US-09-282-505-2   | Sequence 2, Appli  |
| 20         | 1223   | 43.1        | 451    | 3 US-09-054-255-2   | Sequence 2, Appli  |
| 21         | 1223   | 43.1        | 451    | 3 US-09-296-005-14  | Sequence 14, Appli |
| 22         | 1223   | 43.1        | 451    | 3 US-09-296-005-16  | Sequence 16, Appli |
| 23         | 1223   | 43.1        | 451    | 3 US-09-296-005-18  | Sequence 18, Appli |
| 24         | 1223   | 43.1        | 451    | 4 US-09-282-846-2   | Sequence 2, Appli  |
| 25         | 1223   | 43.1        | 451    | 4 US-09-680-145-2   | Sequence 14, Appli |
| 26         | 1223   | 43.1        | 451    | 4 US-09-920-171-14  | Sequence 16, Appli |
| 27         | 1223   | 43.1        | 451    | 4 US-09-920-171-16  | Sequence 16, Appli |

## RESULT 1

US-07-613-083B-1

; Patent No. 5340727

## GENERAL INFORMATION:

; APPLICANT: Ruggeri, Zaverio M.

; APPLICANT: Ware, Jerry, inventors

; APPLICANT: on behalf of Scripps Clinic and Research

; APPLICANT: Foundation

; TITLE OF INVENTION: GPIB: Fragments and Recombinant

; TITLE OF INVENTION: DNA Expression Vectors

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scripps Clinic and Research

; ADDRESS: Foundation

; STREET: 10666 No. 5340727th Torrey Pines Road

; CITY: La Jolla

; STATE: California

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette-5.25 inch, 1.2 Mb

; COMPUTER: AST Bravo IBM PC comp. (386SX)

; OPERATING SYSTEM: MS DOS version 3.2

; SOFTWARE: WordPerfect 5.1 conv. to ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/613,083B

; FILING DATE: 19911114

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA: This appl. is a c-i-p of

; APPLICATION NUMBER: U.S. 07/470,674

; FILING DATE: 04-Jan-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Barron, Alexis

; REGISTRATION NUMBER: 22,702

; REFERENCE/DOCKET NUMBER: P16,569-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 923-3466

; TELEFAX: (215) 923-2189

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 320

; TYPE: AMINO ACID

; STRANDEDNESS: No. 5340727 applicable

; TOPOLOGY: Linear

; US-07-613-083B-1

; Query Match Score 1528.5; DB 1; Length 320;

; Best Local Similarity 95.1%; Pred. No. 6.8e-129;

; Matches 291; Conservative 1; Mismatches 3; Index 11; Gaps 1;

Qy 17 HPICEVSKVASHLEVNCDKRNLTALPPDLPKDTTLIHLSENLLYTFSLATLMPYTRLTLQ 76  
 Db 1 HPICEVSKVASHLEVNCDKRNLTALPPDLPKDTTLIHLSENLLYTFSLATLMPYTRLTLQ 60  
 Qy 77 NLDRCLELTKLOYDTGLPVLGTLPSNQLQSLPLIGQTLPAITLVDVSFNRLTSLPLGAL 136  
 Db 61 NLDRCLELTKLOYDTGLPVLGTLPSNQLQSLPLIGQTLPAITLVDVSFNRLTSLPLGAL 120  
 Qy 137 RGLGEIQLQELYLGKNEIQLTPKLEKSLIANNNTTELPAGLLNGIENLDTLILQ 196  
 Db 121 RGLGEIQLQELYLGKNEIQLTPKLEKSLIANNNTTELPAGLLNGIENLDTLILQ 180  
 Qy 197 ENSLYTIPKGPGFSGHLLPAPLHGNCNLCEILYFRMQLQDNAANVYTKQVQDVKAVT 256  
 Db 181 ENSLYTIPKGPGFSGHLLPAPLHGNCNLCEILYFRMQLQDNAANVYTKQVQDVKAVT 240  
 Qy 257 SVA SVQCDNSDKFPVYKYPKGCPGCPGTLGDEGDTDLYDYPEEDTEGDKR----- 306  
 Db 241 SVA SVQCDNSDKFPVYKYPKGCPGCPGTLGDEGDTDLYDYPEEDTEGDKRATRTRVVKFPT 300  
 Qy 307 -PHTCP 311  
 Db 301 KAHTTP 306

RESULT 2  
 US-07-821-717B-6  
 Sequence 6, Application US/07821717B  
 ; Patent No. 598239  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miller, Jonathan L.  
 ; CUNNINGHAM, David  
 ; APPLICANT: Lyle, Vicki A.  
 ; APPLICANT: Finch, Clara N.  
 ; TITLE OF INVENTION: MUTATIONS RENDERING PLATELET  
 ; TITLE OF INVENTION: GLYCOPROTEIN IB ALPHA LESS REACTIVE  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
 ; STREET: Clinton Square, P.O. Box 1051  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/821,717B  
 ; FILING DATE: 15-JAN-1992  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Timain, Susan J.  
 ; REGISTRATION NUMBER: 34,103  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (716) 263-1636  
 ; TELEFAX: (716) 263-1600  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 610 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PUBLICATION INFORMATION:  
 ; AUTHORS: Lopez, Jose A.  
 ; AUTHORS: Chung, Dominic W.  
 ; AUTHORS: Fujikawa, Kazuo  
 ; AUTHORS: Hagan, Frederick S.

RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 610  
 PUBLICATION DATE: AUG-1987  
 AUTHORS: Zimmerman, Theodore S.  
 AUTHORS: Ruggeri, Zaverio M.  
 AUTHORS: Houghton, Richard A.  
 AUTHORS: Vincente, Vincente  
 AUTHORS: Mohri, Hiroshi  
 TITLE: Proteolytic fragments and synthetic  
 TITLE: Peptides that block the binding of von Willebrand factor to the  
 TITLE: Platelet membrane glycoprotein Ib  
 DOCUMENT NUMBER: EP 0 317 278 A2  
 FILING DATE: 16-NOV-1988  
 PUBLICATION DATE: 24-MAY-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 293  
 US-07-822-717B-6

Query Match 53.6%; Score 1521.5; DB 1; Length 610;  
 Best Local Similarity 82.9%; Pred. No. 7.8e-128;  
 Matches 301; Conservative 5; Mismatches 22; Indels 35; Gaps 5;

Qy 17 HPICEVSKVASHLEVNCDKRNLTALPPDLPKDTTLIHLSENLLYTFSLATLMPYTRLTLQ 76  
 Db 1 HPICEVSKVASHLEVNCDKRNLTALPPDLPKDTTLIHLSENLLYTFSLATLMPYTRLTLQ 60  
 Qy 77 NLDRCLELTQVQDGTLPVGLTLDLQHNOQSLPLIGQTLPAITLVDVSFNRLTSLPLGAL 136  
 Db 61 NLDRCLELTQVQDGTLPVGLTLDLQHNOQSLPLIGQTLPAITLVDVSFNRLTSLPLGAL 120  
 Qy 137 RGLGEIQLQELYLGKNEIQLTPKLEKSLIANNNTTELPAGLLNGIENLDTLILQ 196  
 Db 121 RGLGEIQLQELYLGKNEIQLTPKLEKSLIANNNTTELPAGLLNGIENLDTLILQ 180  
 Qy 197 ENSLYTIPKGPGFSGHLLPAPLHGNCNLCEILYFRMQLQDNAANVYTKQVQDVKAVT 256  
 Db 181 ENSLYTIPKGPGFSGHLLPAPLHGNCNLCEILYFRMQLQDNAANVYTKQVQDVKAVT 240  
 Qy 257 SVA SVQCDNSDKFPVYKYPKGCPGCPGTLGDEGDTDLYDYPEEDTEGDKR----- 306  
 Db 241 SVA SVQCDNSDKFPVYKYPKGCPGCPGTLGDEGDTDLYDYPEEDTEGDKRATRTRVVKFPT 300  
 Qy 307 -PHTCP 344  
 Db 361 KST 363

RESULT 3  
 US-08-119-262B-6  
 ; Sequence 6, Application US/08119262B  
 ; Patent No. 549289  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miller, Jonathan L.  
 ; APPLICANT: Cunningham, David  
 ; APPLICANT: Lyle, Vicki A.  
 ; APPLICANT: Finch, Clara N.  
 ; TITLE OF INVENTION: MUTATIONS RENDERING PLATELET  
 ; TITLE OF INVENTION: GLYCOPROTEIN IB ALPHA LESS REACTIVE  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
 ; STREET: Clinton Square, P.O. Box 1051  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 14603

CITY: Rochester  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 14603

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/119, 262B  
 FILING DATE: 09-SEP-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/821, 717  
 FILING DATE: 15-JAN-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Timain, Susan J.  
 REGISTRATION NUMBER: 34,103  
 REFERENCE/DOCKET NUMBER: 20884/22

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (716) 263-1636  
 TELEFAX: (716) 263-1600

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 610 amino acids  
 TYPE: amino acid  
 STRAINDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

PUBLICATION INFORMATION:  
 AUTHORS: Lopez, Jose A.  
 AUTHORS: Chung, Dominic W.  
 AUTHORS: Fujikawa, Kazuo  
 AUTHORS: Hagen, Frederick S.  
 AUTHORS: Papayannopoulou, Thalia  
 AUTHORS: Roth, Gerald J.  
 TITLE: Cloning of the alpha chain of human platelet  
 TITLE: Glycoprotein Ib: A transmembrane protein  
 TITLE: leucine-rich alpha-2-glycoprotein

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.  
 VOLUME: 84  
 PAGES: 5615-5619  
 DATE: AUG-1987

RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 610

AUTHORS: Zimmerman, Theodore S.  
 AUTHORS: Ruggieri, Zaverio M.  
 AUTHORS: Houghton, Richard A.  
 AUTHORS: Vincente, Vincente  
 AUTHORS: Mohri, Hiroshi

TITLE: Proteolytic fragments and synthetic peptides  
 that block the binding of von Willebrand  
 factor to the  
 membrane glycoprotein Ib

TITLE: membrane glycoprotein Ib

DOCUMENT NUMBER: EP 0 317 278 A2

FILING DATE: 16-NOV-1988

PUBLICATION DATE: 24-MAY-1989

RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 293

US-08-119,262B-6

Query Match 53.6%; Score 1521.5; DB 1; Length 610;  
 Best Local Similarity 82.9%; Pred. No. 7.8e-128;  
 Matches 301; Conservative 5; Mismatches 22; Indels 35; Gaps 5;

Qy 17 HPICEVSKVASHLEVNCDRNLTALPPDLPKDPTTILHSENLLYTSLATLMPYTRILQ 76  
 1 HPICEVSKVASHLEVNCDRNLTALPPDLPKDPTTILHSENLLYTSLATLMPYTRILQ 60

Qy 77 NLDRCBLTQVQDGTLPVIGTLDSHNOQLSLPLGQTPLALTVTSNRLTSPLGAL 136  
 61 NLDRCBLTQVQDGTLPVIGTLDSHNOQLSLPLGQTPLALTVTSNRLTSPLGAL 120

Qy 137 RGLGELQELYLGKGNELKTLPPGLTPTPKLEKLSLANNNLTLPAGLNGLENLTLQ 196

Db 121 RGLGELQELYLGKGNELKTLPPGLTPTPKLEKLSLANNNLTLPAGLNGLENLTLQ 180

Qy 197 ENSLYTICKFFGFSHLLPAFLGNPFLCNCCELYFRLWQDNAEYTWKQVVDVKAVT 256  
 Db 181 ENSLYTICKFFGFSHLLPAFLGNPFLCNCCELYFRLWQDNAEYTWKQVVDVKAVT 240

Qy 257 SNTAVSQCDNSDKFPVVKYKPGKRCPTLGDEGDTDLYDYPEEDEGDKVR----- 306

Db 241 SNTAVSQCDNSDKFPVVKYKPGKRCPTLGDEGDTDLYDYPEEDEGDKVRATRTVVKFPT 300

Qy 307 -PTTCP-----PCPA-----PEALGAPSVPFLFPPK -PKDTL-----MISRTP 341  
 Db 301 KAHTTPMGLFYSMSTSASLDSDQMPSSLHPTQESTKEQTTPRPTNFTLHMESTTFSKTP 360

Qy 342 EVT 344  
 Db 361 KST 363

RESULT 4  
 US-08-135-929A-11  
 Sequence 11, Application US/08135929A  
 ; Patent No. 5593959

GENERAL INFORMATION:  
 ; APPLICANT: Miller, Jonathan L.  
 ; APPLICANT: Cunningham, David  
 ; APPLICANT: Lyle, Vicki A.  
 ; APPLICANT: Finch, Clara N.  
 ; APPLICANT: Pinicus, Matthew R.  
 ; TITLE OF INVENTION: Mutations in the Gene Encoding the Alpha  
 ; Glycoprotein Ib  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
 ; STREET: Clinton Square, P.O. Box 1051  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/135,929A  
 ; FILING DATE: 14-OCT-1993  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Timain, Susan J.  
 ; REGISTRATION NUMBER: 34,103  
 ; REFERENCE/DOCKET NUMBER: 20884/23  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (716) 263-1636  
 ; TELEFAX: (716) 263-1600  
 ; TELEX: 978450  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 610 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-135-929A-11

Qy 17 HPICEVSKVASHLEVNCDRNLTALPPDLPKDPTTILHSENLLYTSLATLMPYTRILQ 76  
 1 HPICEVSKVASHLEVNCDRNLTALPPDLPKDPTTILHSENLLYTSLATLMPYTRILQ 60

Qy 17 HPICEVSKVASHLEVNCDRNLTALPPDLPKDPTTILHSENLLYTSLATLMPYTRILQ 76  
 1 HPICEVSKVASHLEVNCDRNLTALPPDLPKDPTTILHSENLLYTSLATLMPYTRILQ 60

RESULT 5  
US -08-234-265A-11  
Sequence 11, Application US/08234265A  
GENERAL INFORMATION:  
APPLICANT: Miller, Jonathan L.  
APPLICANT: Cunningham, David  
APPLICANT: Lyle, Vicki A.  
APPLICANT: Finch, Clara N.  
APPLICANT: Pincus, Matthew R.  
TITLE OF INVENTION: Mutations in the Gene Encoding the 'Chain of Platelet Glycoprotein Ib'  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,265A  
FILING DATE: 28-APR-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Timian, Susan J.  
REGISTRATION NUMBER: 34,103  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 610 amino acids  
TYPE: amino acid  
TOPOLogy: linear  
MOLECULE TYPE: protein  
US -08-234-265A-11

Query 7 NLDRCETKLQVDGTLPVGLTDLSHNQSLPLGOTLPALTVDSENRLTSLUPGAL 136  
Db 61 NLDRCETKLQVDGTLPVGLTDLSHNQSLPLGOTLPALTVDSENRLTSLUPGAL 120  
Query 137 RGLGELQOLYLGKNEKLTQPLTPPLEKLSLANNNLTEPLGQNGLENLDTLLQ 196  
Db 121 RGLGELQOLYLGKNEKLTQPLTPPLEKLSLANNNLTEPLGQNGLENLDTLLQ 180  
Query 197 ENSLYTLPKGFFGSHLIPFAFLHGNPWLNCNCBILYFRWILQDNAENVYWKQVVDVKAVT 256  
Db 181 ENSLYTLPKGFFGSHLIPFAFLHGNPWLNCNCBILYFRWILQDNAENVYWKQVVDVKAVT 240  
Query 257 SVAASYCDNSPDKPYPKYPGKCPPLGDEGTDLIDYYPFEDTEGDKVR - - - - 306  
Db 241 SVAASYCDNSPDKPYPKYPGKCPPLGDEGTDLIDYYPFEDTEGDKVR - - - - 306  
Db 242 EVT 344  
Db 361 KST 363

RESULT 6  
US -08-713-556F-36  
Sequence 36, Application US/08713556F  
Patent No. 6277975  
GENERAL INFORMATION:  
APPLICANT: Larsen, Glenn  
APPLICANT: Sako, Dianne  
APPLICANT: Chang, Xiao Jia  
APPLICANT: Veldman, Geertruida M.  
APPLICANT: Cumming, Dale  
APPLICANT: Kumar, Rayindra  
APPLICANT: Shaw, Gray  
TITLE OF INVENTION: NOVEL P-SELECTIN LIGAND PROTEIN  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEGAL AFFAIRS  
STREET: 87 CAMBRIDGE PARK DRIVE  
CITY: CAMBRIDGE  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/713,556F  
FILING DATE: 23-OCT-1992  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,662  
FILING DATE: 26-AUG-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10168  
FILING DATE: 22-OCT-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,608  
FILING DATE: 28-APR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,398  
FILING DATE: 28-APR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10168  
FILING DATE: 22-OCT-1993

Query Match 53.6%; Score 1521.5; DB 1; Length 610;  
Best Local Similarity 82.9%; Pred. No. 7.8e-128;  
Matches 301; Conservative 5; Mismatches 22; Indels 35; Gaps 5;

APPLICATION NUMBER: US 08/316,305  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/428,734  
 FILING DATE: 25-APR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWN, SCOTT A.  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: GI 5213F  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEX/FAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 313 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US 08-713-556-F-36

Query Match 43.6%; Score 1237; DB 3; Length 313;  
 Best Local Similarity 97.0%; Pred. No. 1e-102; Indels 0; Gaps 0;  
 Matches 229; Conservative 0; Mismatches 7;

Qy 296 PEEDEGDKVPRHTCPCCPAAPEALGASVFLPPPKPKDTLMISRTPVTCVVVDVSHEDP 355  
 Db 78 PESTTVEPARHTCPCCPAAPEALGASVFLPPPKPKDTLMISRTPVTCVVVDVSHEDP 137

Qy 356 EVKENVVYDGEVHNATKTPREQQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPVP 415  
 Db 138 EVKENVVYDGEVHNATKTPREQQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPVP 197

Qy 416 IEETISKARGQPREPQVTLPPREEMTKNOVSLLTCLVKGFPYPSDIAVEWEENGOPENNY 475  
 Db 198 IEETISKARGQPREPQVTLPPREEMTKNOVSLLTCLVKGFPYPSDIAVEWEENGOPENNY 257

Qy 476 KITPPVLDSDGSPLFLYSKLTVDKSRWQOQGNVPSCSVMHEALHNHYTOKSLSLSPGK 531  
 Db 258 KITPPVLDSDGSPLFLYSKLTVDKSRWQOQGNVPSCSVMHEALHNHYTOKSLSLSPGK 313

RESULT 8  
 US-09-784-623-16

Qy 226 NCIBILYPRRMQDNAAVYVVKQVVDYKAVTSNVAVQCDNSDKFPVYKYPKGCP----  
 Db 69 SCYTKSGDTRQLLEAN----ITDLSENRKDKRFAFIRSDGGPTTSFESAACPWFL 122

Qy 282 ----TLDGEGDTDLYDYPEEDETEGD----KVRPHTCPPCPAAPEALGAPSVF 325  
 Db 123 CTAMEADOPVSLTNMPDEGMVYTKFQDEAAEPKSSDTHTCPPCPAPLLGGSVVF 182

Qy 326 LFPPPKPDTLMSRTPEVTCVVVDVSHEDPEVTKFNTYDGEVHNATKTPREEQYNSTYR 385  
 Db 183 LFPPPKPDTLMSRTPEVTCVVVDVSHEDPEVTKFNTYDGEVHNATKTPREEQYNSTYR 242

Query Match 43.3%; Score 1230; DB 3; Length 388;  
 Best Local Similarity 64.5%; Pred. No. 5.9e-102; Mismatches 69; Indels 48; Gaps 6;  
 Matches 249; Conservative 20; Mismatches 65;

Qy 171 LANNLTELPAULNG----LENLDTLQENSLLTIPKGFFGSHLIPFPLHGNPWL 225  
 Db 26 LRNN--OLVAGYLQGPVNVLKEKIDVPIEPHAL----ITDLSENRKDKRFAFIRSDGGPTTSFESAACPWFL 122

Qy 226 NCIBILYPRRMQDNAAVYVVKQVVDYKAVTSNVAVQCDNSDKFPVYKYPKGCP----  
 Db 69 SCYTKSGDTRQLLEAN----ITDLSENRKDKRFAFIRSDGGPTTSFESAACPWFL 122

Qy 282 ----TLDGEGDTDLYDYPEEDETEGD----KVRPHTCPPCPAAPEALGAPSVF 325  
 Db 123 CTAMEADOPVSLTNMPDEGMVYTKFQDEAAEPKSSDTHTCPPCPAPLLGGSVVF 182

Query Match 43.3%; Score 1230; DB 3; Length 388;  
 Best Local Similarity 64.5%; Pred. No. 5.9e-102; Mismatches 20; Mismatches 65; Indels 48; Gaps 6;  
 Matches 249; Conservative 20; Mismatches 65;

Qy 181 LANNLTELPAULNG----LENLDTLQENSLLTIPKGFFGSHLIPFPLHGNPWL 225  
 Db 171 LANNLTELPAULNG----LENLDTLQENSLLTIPKGFFGSHLIPFPLHGNPWL 225

RESULT 9  
 US-08-897-236-23  
 ; Sequence 23, Application US/0897236A  
 ; Patent No. 6075007  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Regeneron Pharmaceuticals, Inc. Modified Dorsal Tissue Affecting Factor and Composition  
 ; TITLE OF INVENTION: Modified Dorsal Tissue Affecting Factor and Composition  
 ; FILE REFERENCE: REG 133  
 ; CURRENT APPLICATION NUMBER: US/08/897,236A  
 ; CURRENT FILING DATE: 1997-07-17  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 23  
 ; LENGTH: 449  
 ; TYPE: PRT  
 ; ORGANISM: human  
 ; US-08-897-236-23

Query Match 43.3%; Score 1230; DB 3; Length 449;  
 Best Local Similarity 56.1%; Pred. No. 7.4e-102;  
 Matches 21; Mismatches 95; Gaps 13;  
 Indels 98; Gaps 13;

Qy 105 LQSLPLGQTLPAITVLDVSFRNLTSPLGSLRGL-----  
 Db 1 MERCPSLGLRSLGGHDPGMATSPPEDRPGGGG-----  
 Qy 140 -GELOELYLGKNEKTLPLPGLLTPPKLEKLSLANNNLTELPAGLNGLENLDLLOE 139  
 Db 57 KEKDNEETLRLRSLLGGHDPGMATSPPEDRPGGGG-----  
 Qy 198 NSLYTIPKGFFGSHLIPFAFLHG----NPWLCN---CEILYFRWLQDNAENTYVWKQV 249  
 Db 112 ----PSGAMPSEIKGLFSEGIAQGLQMLWQTCFPLVY-AW---NDLGSRFWPKY 160  
 Qy 250 VDV-----  
 Db 161 VKVGSCFSKRSCSVPEGMVKPSVSHLTLRWRQ-----  
 Qy 290 DLYDYP----EPTEGDKVRPHTCPPCPAPPAAGAPSVLFLPPKPKDOLMISRTPEYT 289  
 Db 210 ----YPIITSECKCSGDKT-HTCPCPAPELGGPSVFLFPKPKDOLMISRTPEYT 262  
 Qy 345 CWNVDYSHDPEVKENWYDGVYHNAKTKPREFQYNSTYRVSVLTVLHQDWLNGKEYK 404  
 Db 263 CWNVDYSHDPEVKENWYDGVYHNAKTKPREFQYNSTYRVSVLTVLHQDWLNGKEYK 322  
 Qy 405 CKVSNKALPVPIEKTKAKGQPREPVYTLPPREEMTKQVSLTCLVKGFYPSDIAVE 464  
 Db 323 CKVSNKALPVPIEKTKAKGQPREPVYTLPPREEMTKQVSLTCLVKGFYPSDIAVE 382  
 Qy 465 WESNGOPENNYKTTIPVLDGSFFLSDGSFLYSLTVKSRQOGNVSFSVMMHEALHNHYTQKS 524  
 Db 383 WESNGOPENNYKTTIPVLDGSFFLSDGSFLYSLTVKSRQOGNVSFSVMMHEALHNHYTQKS 442  
 Qy 525 LSLSPGK 531  
 Db 443 LSLSPGK 449

RESULT 11  
 US-08-77-066-2  
 ; Sequence 2, Application US/08775066  
 ; Patent No. 662013  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Desauvage, Frederic  
 ; APPLICANT: Levin, Nancy  
 ; TITLE OF INVENTION: Ob protein-immunoglobulin chimeras  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California

COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/775,066  
 FILING DATE: 27-Dec-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Ginger R.  
 REGISTRATION NUMBER: 33,055  
 REFERENCE/DOCKET NUMBER: P0985R1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-3216  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 397 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-775-066-2

Query Match 43.2%; Score 1226.5; DB 4; Length 397;  
 Best Local Similarity 66.0%; Pred. No. 1.3e-10;  
 Matches 256; Conservative 17; Mismatches 48; Indels 67; Gaps 9;

Qy 157 SHLPPAPLHGPNWLNCILYFRRWLQDNAENVY----VVKQVVDYKAVTSNVASV-Q 263  
 Db 64 PGLHPILTLKMDQTLAVYQQLITSMSPRNVIQISNDLENRLD---- 108

Qy 210 SHLPPAPLHGPNWLNCILYFRRWLQDNAENVY----VVKQVVDYKAVTSNVASV-Q 263  
 Db 109 -HYLAFSKSKSCHLWASGJBLT----DSLGSVLEASGSYSTEVALSRLQGSQSLQMLWQ 160

Qy 264 CDNSDKPPVYKPGCGCPTLGDEGDTPLDYKPFEDTEGDKVRPHTCPPCAPEAGAPS 323  
 Db 161 LDLS----PGC----GVTD----KHTTCPCPAPELGGPS 189

Qy 324 VFLPPKRDTLMSRTPVBTCVVVDYSHEDPEPVKFWYVGDGEVHNAKTKEEQYNST 383  
 Db 190 VFLPPKRDTLMSRTPVBTCVVVDYSHEDPEVKFWYVGDGEVHNAKTKEEQYNST 249

Qy 384 YRVSVLTVLHQDWLNGKEYKCKVSKNPKALPVPIETKTSKAKCOPREPOVYTLPPSREEMT 443  
 Db 250 YRVSVLTVLHQDWLNGKEYKCKVSKNPKALPAPIETKTSKAKCOPREPOVYTLPPSREEMT 309

Qy 444 KNOVSLTCLVKGPGYPSDAAVENEWSNGQDPENNNTKTPVLDSDGSFFLYSKLT 503  
 Db 310 KNQVSLTCLVKGPGYPSDAAVENEWSNGQDPENNNTKTPVLDSDGSFFLYSKLT 369

Qy 504 GNFSCSYWHEALHNHYTQKSLSLSPGK 531  
 Db 370 GNFSCSYWHEALHNHYTQKSLSLSPGK 397

RESULT 12  
 US-08-887-352B-14  
 Sequence 14, Application US/088887352B  
 ; Patent No. 5994511  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
 ; TITLE OF INVENTION: Improving Polypeptides  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA

RESULT 13  
 US-08-887-352B-16  
 Sequence 16, Application US/088887352B  
 ; Patent No. 5994511  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
 ; TITLE OF INVENTION: Improving Polypeptides  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA

ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Win95tin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
SEQUENCE CHARACTERISTICS: 16:  
LENGTH: 451 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
-08-387-352B-16

RESULT 14  
-08-887-352B-18  
Sequence 18, Application US/08887352B  
Patent No. 5994511  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowrie  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
TITLE OF INVENTION: Improving Polypeptides  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
S-08-887-352B-18

| Query Match           | 43.1%   | Score 1223;                             | DB 2;      | Length 451; |
|-----------------------|---|---|------------|-------------|
| Best Local Similarity | 64.1%   | Pred. No. 3..2e10;                      |            |             |
| Matches 254;          | Conservative 14;  | Missmatches 58;                         | Indels 70; | Gaps 10;    |
| Y                     | 188 ENLDLTLIQLQENSILYTPKGFF   | ---GSHLPPAFALHGNPWLNCNCEILYPRRMQLQDNENV | 243        |             |
| b                     | 74 DSKNTFTYLQMNSLSLRAEDFAYVYCARSHY                                  | ----FGH----W-----                       | 119        |             |
| Y                     | 244 YWKQCVVDFYKAVTSNVAVSYCQDNSDKFIP                                 | -----VYKPGKGC                           | 280        |             |
| b                     | 120 SSASTKGPSVFPLAPPSKSTSGTAAAGCLVRDYFPPEPVTSWNSGALTSGWHTFPAA       | --:                                     | 176        |             |
| Y                     | 281 PTGIDEG   | -----DTDLY-----DYYPERDTEGDKVPRP-----    | 315        | -HTCPICCPA  |
| b                     | 177 -VLSQSGLYSLSSVVTVPSSSLQTQYICAVNWKHPSPNTKVDKVKPEPKSDKDHHTCPICCPA | 235                                     |            |             |
| Y                     | 316 PEALGAPSVLFLPPKPKDITLMSRTPEVTCVYDVSHEDPEVKFNYYDGVYEVHNAKTKP     | 375                                     |            |             |
| b                     | 236 PELLGGPSVLFLPPKPKDITLMSRTPEVTCVYDVSHEDPEVKFNYYDGVYEVHNAKTKP     | 295                                     |            |             |
| Y                     | 376 REEQYNSTYRVSVLTVLHQDWLNGKEYKCKVYSNKAALPVPIEKTISAKGQPREPVQYTL    | 435                                     |            |             |
| b                     | 296 REEQYNSTYRVSVLTVLHQDWLNGKEYKCKVYSNKAALPAPIEKTISAKGQPREPVQYTL    | 355                                     |            |             |
| Y                     | 436 PPSREEMTKQNOVSLTCLYKGFYFSDIAVEWENQOPENNYKTPVLDSDSSFLFLSKLT      | 495                                     |            |             |
| b                     | 356 PPSREEMTKQNOVSLTCLYKGFYFSDIAVEWENQOPENNYKTPVLDSDSSFLFLSKLT      | 415                                     |            |             |
| Y                     | 496 VDKSRWQGNVFSCSMHEALHNHYTKSLSLSPGK                               | 531                                     |            |             |
| b                     | 416 VDKSRWQGNVFSCSMHEALHNHYTKSLSLSPGK                               | 451                                     |            |             |

RESULT 15  
S-08-466-151-65  
Sequence 65 Application US/08466151  
Patent No. 6037453  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM.

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genantech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,151  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/466163  
 FILING DATE: 06-Jun-1995  
 APPLICATION NUMBER: 08/405617  
 FILING DATE: 15-MAR-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/185899  
 FILING DATE: 26-JAN-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 07/879495  
 FILING DATE: 07-MAY-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 07/744768  
 FILING DATE: 14-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svoboda, Craig G.  
 REGISTRATION NUMBER: 39,044  
 REFERENCE/DOCKET NUMBER: P0718P2C1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 65:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 451 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-466-151-65

Query Match 43.11: Score 1223; DB 3  
 Best Local Similarity 64.11; Pred. No. 3 2e-10  
 Matches 254; Conservative 14; Mismatches 5

|     |     |   |                       |
|-----|-----|---|-----------------------|
| Qy  | 188 | ENLDLTLQIENSUYTIPKGFF                   | ----GSHLPLPAFLIGC     |
| Ddb | 74  | DSKNTFVYQMNLSRAEDTAVYTCGSHY             | ---- -FGH             |
| Qy  | 244 | -----YWWKQVVDIKAFTSNVAVSQCDNSDKFP       |                       |
| Ddb | 120 | SSASTKGPSVFPLAASSKTSSTGSGTAALGCLVRYDFP  |                       |
| Qy  | 281 | PTLGDEG                                 | -----DTDLY-----DTYPEE |
| Ddb | 177 | -VILOSSGLYSLSSVTVTPSSSLQATQYTCIYVNHKPSN |                       |
| Qy  | 316 | PEALGAPSYVFLPPPKPKDTIMISRTPTVTCVYDVSH   |                       |
| Ddb | 236 | PELIGGSPVFLPPPKPKDTIMISRTPTVTCVYDVSH    |                       |
| Qy  | 376 | REEOYNSTYRVSVLTVJHDQWINGKRYKCKVSNKAI    |                       |
| Ddb | 296 | REEOYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKAI    |                       |
| Qy  | 436 | PPSRMEETKNOVSLTCVYKGPYPSDIAVEMWSNGOP    |                       |
| Ddb | 356 | PPSRMEETKNOVSLTCVYKGPYPSDIAVEMWSNGOP    |                       |
| Qy  | 496 | VDKSRWQOGNVPSCSVWMBALINHYTKSLSLSLSPGK   |                       |
| Ddb | 416 | VDKSRWQOGNVPSCSVWMBALINHYTKSLSLSLSPGK   |                       |

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GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: May 24, 2005, 05:54:10 ; Search time 42 Seconds  
(without alignments)  
1215.455 Million cell updates/sec

Title: US-10-068-426-5

Perfect score: 2839  
Sequence: 1 MPLIILLLLPSPLHPICT.....MHEALHNHYTQKSLSLSPGK 531

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query | Match | Length | DB     | ID | Description                            |
|------------|--------|-------|-------|--------|--------|----|--|
| 1          | 1615.5 | 56.9  | 626   | 1      | NBHUTA |    | platelet glycoprotein Ib alpha chain C |
| 2          | 1205   | 42.4  | 330   | 1      | GHHU   |    | Ig gamma-1 chain C                     |
| 3          | 1203   | 42.4  | 374   | 2      | S69339 |    | Ig heavy chain V                       |
| 4          | 1197   | 42.2  | 255   | 4      | S31866 |    | Ig gamma-1 chain C                     |
| 5          | 1152   | 40.6  | 234   | 2      | PT0207 |    | Ig gamma chain C r                     |
| 6          | 1148   | 40.4  | 326   | 1      | G2HU   |    | Ig gamma-2 chain C                     |
| 7          | 1145   | 40.3  | 377   | 2      | A23511 |    | Ig gamma-3 chain C                     |
| 8          | 1143   | 40.3  | 327   | 1      | A60764 |    | Ig gamma-3 chain C                     |
| 9          | 1134   | 40.0  | 39    | 1      | G4HU   |    | Ig gamma-4 chain C                     |
| 10         | 1116   | 39.3  | 289   | 1      | G3H0WI |    | Ig gamma-3 heavy C                     |
| 11         | 921    | 32.4  | 323   | 1      | GHRB   |    | Ig gamma chain C r                     |
| 12         | 913    | 32.2  | 328   | 2      | A17160 |    | Ig gamma 2b chain                      |
| 13         | 913    | 32.2  | 328   | 2      | 147159 |    | Ig gamma 2a chain                      |
| 14         | 906    | 31.9  | 277   | 2      | I47162 |    | Ig gamma 4 chain C                     |
| 15         | 893    | 31.5  | 328   | 2      | I47158 |    | Ig gamma 1 chain C                     |
| 16         | 884    | 31.5  | 328   | 2      | G2GP   |    | Ig gamma-2 chain C                     |
| 17         | 881    | 31.0  | 328   | 2      | I47161 |    | Ig gamma 3 chain C                     |
| 18         | 857    | 30.5  | 470   | 2      | S22080 |    | Ig heavy chain pre                     |
| 19         | 849    | 29.9  | 308   | 2      | C30524 |    | Ig heavy chain C r                     |
| 20         | 849    | 29.9  | 472   | 2      | S3159  |    | Ig gamma-1 chain C                     |
| 21         | 841    | 29.6  | 329   | 1      | G3MSC  |    | Ig gamma 3 chain C                     |
| 22         | 838    | 29.5  | 444   | 2      | PC4436 |    | monoclonal antibody                    |
| 23         | 834    | 29.4  | 326   | 2      | PS0017 |    | Ig gamma-1 chain C                     |
| 24         | 830    | 29.2  | 398   | 1      | G3MSM  |    | Ig gamma 3 chain C                     |
| 25         | 828    | 29.1  | 324   | 1      | G1MS   |    | Ig gamma-1 chain C                     |
| 26         | 826    | 29.1  | 333   | 2      | PS0018 |    | Ig gamma-2b chain                      |
| 27         | 821    | 28.9  | 329   | 2      | S00847 |    | Ig gamma-2c chain                      |
| 28         | 821    | 28.9  | 393   | 2      | G1MSM  |    | Ig gamma-1 chain C                     |
| 29         | 817    | 28.8  | 322   | 2      | PS0019 |    | Ig gamma-2a chain                      |

#### RESULT 1

NBHUTA

platelet glycoprotein Ib alpha chain precursor - human

N:Alternate names: membrane Glycoprotein Ib alpha chain

N:Contains: glyccocalicin

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004

C:Accession: A94174; A60435; I64173; S16345; A27075; A27102

R: Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J. Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987

A:Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane protein

A:Reference number: A94174; MUID:303030

A:Molecule type: mRNA

A:Residues: 1-626 <WIC>

A:Cross-references: UNIPROT: P07359; GB: J02940; PIDN: AA52595-1; PMID: 9306793

R: Wicki, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.; Clemetson, K.J. Thromb. Haemost. 61, 448-453, 1989

A:Title: Isolation and characterization of human blood platelet mRNA and construction of a cDNA insert.

A:Reference number: A60435; MUID: 90020160; PMID: 2799758

A:Accession: A60435

A:Molecule type: protein

A:Residues: 1-715 <WIC>

R: Titani, K.; Tokio, K.; Handa, M.; Ruggeri, Z.M. Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987

A:Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet memt

A:Reference number: A94173; MUID: 3497398

A:Accession: A94173

A:Molecule type: protein

A:Residues: 1-715 <WIC>

R: Hess, D.; Schaller, B.E.; Clemetson, K.J. Eur. J. Biochem. 199, 389-393, 1991

A:Title: Identification of the disulphide bonds in human platelet glyccocalicin.

A:Reference number: S16945; MUID: 91301149; PMID: 2070794

A:Accession: S16945

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 224-227-262-270-277-282 <HES>

R: Lopez, J.A.; Ludwig, B.H.; McCarthy, B.J. J. Biol. Chem. 267, 10055-10051, 1992

A:Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of tte

A:Residues: 1-315

A:Accession: 155355; MUID: 92250564; PMID: 1577776

A:Reference number: I55355

A:Status: Preliminary; translated from GB/EMBL/DDJB

A:Molecule type: DNA

A:Residues: 412-427 <RES>

A:Cross-references: GB: S34436; PIDN: AAB22152-1; PMID: 3249177

A:Note: variant D

C:Comment: Glycoprotein Ib (GP1b), a surface membrane protein of platelets, participates

C:Comment: Platelet activation apparently involves disruption of the macromolecular comp



|   |     |  |   |     |
|---|-----|--|---|-----|
| F:137-206/Domain: immunoglobulin homology <IM2>   | Qy  | 426  | QPREPOVYTLPSSREMTKQVSLLTCLVKGKFYPSDIAVEWSNGOPENNYKTTTPVLDSD | 485 |
| F:243-310/Domain: immunoglobulin homology <IM3>   | Db  | 269  | QPREPVYTLPSSREMTKQVSLLTCLVKGKFYPSDIAVEWSNGOPENNYKTTTPVLDSD  | 328 |
| F:27-81,144-204,305-308/Disulfide bonds: #status experimental                                     |     |  |   |     |
| F:103/Disulfide bonds: interchain (to light chain) #status experimental                           | Qy  | 486  | GSFFLYSKLTVDKSRROQNYFSCSYNHEALHNHYTOKSLSLSPGK               | 531 |
| F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental                       | Db  | 329  | GSFFFLSKLTVDKSRROQNYFSCSYNHEALHNHYTOKSLSLSPGK               | 374 |
| F:180/Binding site: carbonylate (Asn) (covalent) #status experimental                             |     |  |   |     |
| Query Match   |     |  |   |     |
| Best Local Similarity 42.4%; Score 1205; DB 1;  |     |  |   |     |
| Matches 235; Conservative 10; Mismatches 30; Indels 4; Gaps 5;                                    |     |  |   |     |
| RESULT 4  |     |  |   |     |
| S31866  |     |  |   |     |
| 19 gamma-1 chain C region - synthetic   |     |  |   |     |
| C;Species: synthetic  |     |  |   |     |
| A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli                      |     |  |   |     |
| C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000                       |     |  |   |     |
| C;Accession: S31866   |     |  |   |     |
| R;Filipula, D.  |     |  |   |     |
| Submitted to the EMBL Data Library, February 1993   |     |  |   |     |
| A;Description: Screening method for protein-protein interactions of cloned gene products.         |     |  |   |     |
| A;Reference number: S31866  |     |  |   |     |
| A;Accession: S31866   |     |  |   |     |
| A;Molecule type: mRNA   |     |  |   |     |
| A;Residues: 1-255 <FLN>   |     |  |   |     |
| A;Cross-references: EMBL:X70421; NID:933068; PIDN:CAA49866-1; PID:933069                          |     |  |   |     |
| C;Keywords: immunoglobulin  |     |  |   |     |
| F:1-224/Region: Escherichia coli outer membrane protein A precursor                               |     |  |   |     |
| F:23-355/Region: human Ig gamma-1 chain C region  |     |  |   |     |
| Query Match   |     |  |   |     |
| Score 1197; DB 4; Length 255;   |     |  |   |     |
| Best Local Similarity 96.9%; Pred. No. 2.3e-73;   |     |  |   |     |
| Matches 219; Conservative 3; Mismatches 4; Indels 0; Gaps 0;                                      |     |  |   |     |
| Qy  | 306 | RPHTCPCCPAPAEALGAPSVLFLPPPKDPTLMSRTPEVTCVVDVSHEDPEVKFNWYD  | 365   |     |
| Db  | 30  | KTHTCPCCPAPAEALGAPSVLFLPPPKDPTLMSRTPEVTCVVDVSHEDPEVKFNWYD  | 89  |     |
| Qy  | 366 | VEVHNAKTKPKEQYNTSYRVSVLTVLHQDWLNGKEYKCKVSNKALPVPIKTTISKAG  | 425   |     |
| Db  | 90  | VEVHNAKTKPKEQYNTSYRVSVLTVLHQDWLNGKEYKCKVSNKALPVPIKTTISKAG  | 149   |     |
| Qy  | 426 | QPREPVYTLPSSREMTKQVSLLTCLVKGKFYPSDIAVEWSNGOPENNYKTTTPVLDSD | 485   |     |
| Db  | 150 | QPREPVYTLPSSREMTKQVSLLTCLVKGKFYPSDIAVEWSNGOPENNYKTTTPVLDSD | 209   |     |
| Qy  | 486 | GSFFFLSKLTVDKSRROQNYFSCSYNHEALHNHYTOKSLSLSPGK              | 531   |     |
| Db  | 210 | GSFFFLSKLTVDKSRROQNYFSCSYNHEALHNHYTOKSLSLSPGK              | 255   |     |
| RESULT 5  |     |  |   |     |
| PT0207  |     |  |   |     |
| Ig gamma chain C region - chimpanzee  |     |  |   |     |
| C;Species: Pan troglodytes (chimpanzee)   |     |  |   |     |
| C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999                       |     |  |   |     |
| C;Accession: PT0207   |     |  |   |     |
| R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.   |     |  |   |     |
| Mol. Immunol. 28, 319-322, 1991   |     |  |   |     |
| A;Title: Nucleotide sequence of chimpanzee Ig gamma chain C region; immunoglobulin homology <IMM> |     |  |   |     |
| A;Accession: PT0207; MUID:91287716; PMID:2062315  |     |  |   |     |
| A;Molecule type: mRNA   |     |  |   |     |
| A;Residues: 1-234 <ER>  |     |  |   |     |
| C;Supfamily: immunoglobulin   |     |  |   |     |
| C;Keywords: immunoglobulin homology <IMM>   |     |  |   |     |
| Query Match   |     |  |   |     |
| Score 1152; DB 2; Length 234;   |     |  |   |     |
| Best Local Similarity 93.8%; Pred. No. 2.2e-70;   |     |  |   |     |
| Matches 213; Conservative 3; Mismatches 5; Indels 6; Gaps 1;                                      |     |  |   |     |
| Qy  | 304 | KYRP-----HTCPCPAPAEALGAPSVLFLPPPKDPTLMSRTPEVTCVVDVSHEDPEV  | 357   |     |
| Db  | 8   | KYRPKSCDTHCPAPAEALGAPSVLFLPPPKDPTLMSRTPEVTCVVDVSHEDPEV     | 67  |     |
| Qy  | 366 | VEVHNAKTKPKEQYNTSYRVSVLTVLHQDWLNGKEYKCKVSNKALPVPIKTTISKAG  | 425   |     |
| Db  | 268 | VEVHNAKTKPKEQYNTSYRVSVLTVLHQDWLNGKEYKCKVSNKALPVPIKTTISKAG  | 268   |     |

**RESULT 6**

G2HU

19. Gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 09-Jul-2004

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant regions

A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-26 <ELL>

A;Cross-references: UNIPROT:PO1859; GB:J00554; GB:J0030; NID:932759; PIDN:CA858438.1; F

A;Note: Ly-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A;Residues: '19,'Q,'21-57,'Z,'59,'A,'61-193,'D',195-325 <WAN>

A;Note: Trp-156 is at or near the complement-binding site

R;Connell, G.E.; Parr, D.M.; Hoffmann, T.

C. J. Blochem. 57, 758-767, 1979

A;Title: The amino acid sequences of the three heavy chain constant region domains of a myeloma protein Zie

A;Reference number: A90752; MUID:80001357; PMID:113060

A;Contents: myeloma protein Zie

A;Accession: A90752

A;Molecule type: protein

A;Residues: 1-24, 'E',26-57,'EV,60-85;132-171,'222',175,'B',177-193,'D',195-196,'Q',198-'

A;Contents: this sequence has since been revised

R;Hoffmann, T.; Parr, D.M.

Mol. Immunol. 16, 933-925, 1979

A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin gamma 3 heavy chain constant region gene

A;Reference number: A93132; MUID:80114419; PMID:18920

A;Contents: Zie

A;Accession: A93132

A;Molecule type: protein

A;Residues: 238-275 <HOF>

R;Hoffmann, T.; Parr, D.M.

Biochim. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A;Contents: annotation: Zie, revisions to residues 25, 59, 60, and 264-268

A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidated N-terminus

R;Milstein, C.; Frangione, B.

Nature 221, 145-148, 1969

A;Title: Structural studies of immunoglobulin G.

A;Contents: annotation: A93135; MUID:65064124; PMID:5782707

C;Genetics:

A;Gene: GDB:IGHG3

A;Cross-references: GDB:119339; OMIM:147120

A;Map position: 14q32.33-14q32.33

A;Intron: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;20-85/Domain: immunoglobulin homology <IMM>

F;239-306/Domain: immunoglobulin homology <IM3>

F;27-83,140-200,246-304/Disulfide bonds: interchain (to light chain) #status experimental

F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

A;Cross-references: GDB:119338; OMIM:147110

C;Map position: 14q12.33-14q12.33

C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a single immunoglobulin C region, immunoglobulin homology

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin homology <IM1>

F;20-85/Domain: immunoglobulin homology <IM2>

F;239-306/Domain: immunoglobulin homology <IM3>

F;14/Disulfide bonds: interchain (to light chain) #status experimental

F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.4% Score 1148; DB 1; Length 326;

Best Local Similarity 72.2%; Pred. No. 6.4e-70;

Matches 226; Conservative 18; Mismatches 33; Indels 36; Gaps 6;

Qy 253 KAVTISNVASVQCDNSDKFP-----VYKYP--GKGCPFL-----

Db 16 RSTSSSTAALGCLVQDYFPEPVTVSNSGALTSGHTRFPAVLQSGLYSSSSVYVPSNN 75

Qy 284 -GDBBDPTDLYDYPPEBDTEBDKVRPH---TCPPPAPEALGAPSVELPPPKPKDTLMIS 338

Db 76 FGTQTYTCNVDTHKP-SNTKVDTKVERTKCYCECPAPPVAG-PSVFLPPPKPKDTLMIS 133

Qy 339 RTPETVCVYVDVSHEDPEVFKNWNVYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 398

Db 134 RTPETVCVVDDVSHEDPEVQFNWTVDFGVEVHNAKTKPREEQFNSTFRVSVLTVHODWL 193

Qy 399 NGKEYCKVSKNSNKALPVPIEKTISKAKGQPREPOVYTLPPSREENTKNOVSLSLTCLVKGFPY 458

Db 194 NGKEYTKCKVSKNSNKGLAPIERKTISKKGQPREPOVYTLPPSREENTKNOVSLSLTCLVKGFPY 253

Qy 459 SDIAWEVWNSQOPENNYKTPVLDSDGSFFLYSKLTVTDKSRWQGNYFSCSVWHEALIN 518

Db 254 SDIAWEVWNSQOPENNYKTPVPPMLDSDGSFFLYSKLTVTDKSRWQGNYFSCSVWHEALIN 313

Qy 519 HYTQKSLSLSPGK 531

Db 314 HYTQKSLSLSPGK 326

RESULT 7

A23511

IG gamma-3 chain C region (allootype G3m(b)) - human

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999

C;Accession: A23511

R;Huck, S.; Port, P.; Crawford, D.H.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: co-intron

A;Reference number: A23511; MUID:86148507; PMID:3081877

A;Molecule type: DNA

A;Cross-references: GB:X03604; GB:12958; PID:933070; PIDN:CAA27268.1; PID:9577056

A;Genetics:

A;Gene: GDB:IGHG3

A;Cross-references: GDB:119339; OMIM:147120

A;Map position: 14q32.33-14q32.33

A;Intron: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 40.3% Score 1145; DB 2; Length 377;

Best Local Similarity 64.4%; Pred. No. 1.2e-69;

Matches 230; Conservative 17; Mismatches 56; Indels 54; Gaps 7;

Qy 194 LLOENSLY-----TIPKGFFGSHLPPFAFLHGNNPWLNCCELYFRRMLQDNAENVYWK 247

Db 56 VLQSSGLYLSLSSVTVPSSLGT-----QTYCN-----VNHKPSNTKVDK 96

Qy 248 QVVDVKAVTNSVASY-----QCDNSDKFVKPVYKYPGK-----GCPTLGDGEGDTDLYD 294  
 Db 97 R-VELKTPGDTHTCPRPEPKSCDTPPCPRPEPKSCDTPPCPEPKSCD--- 151

Qy 295 YPEEDTEGKVKRPHTCPRPEPKSCDTPPCPRPEPKSCDTPPCPEPKSCD----- 354  
 Db 152 -----TTPPCPRCPAPELGGPAPVFLPPKPKDTLMISRTPEVTCVVDVSHD 354  
 Qy 355 PEVKFNVYTDGVVHNAKTKPREFQYNSYTRVSVLTVHQDLNGKEYKCKVSNKALP 414  
 Db 201 PEQVKWYTDGVVHNAKTKPREFQYNSYTRVSVLTVHQDLNGKEYKCKVSNKALP 260

Qy 415 PIETKISKKGOPREPOVYTLPPSREEMTKNOVSLLTCLVKGFYPSDIAVEWESNGOPENN 474  
 Db 261 PIETKISKKGOPREPOVYTLPPSREEMTKNOVSLLTCLVKGFYPSDIAVEWESNGOPENN 320

Qy 475 YKTPPPVLDSDGSFPLYSLKSLTVKSRMKGQNVFSCSYVHEALHNHYTKSLSLSPGK 531  
 Db 3221 YNTPPPVLDSDGSFPLYSLKSLTVKSRMKGQNVFSCSYVHEALHNRTQKSLSLSPGK 377

RESULT 8

A6764 Ig gamma-3 chain C region, form LAT - human  
 C;Species: Homo sapiens (man)  
 C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
 R;Huck, S; Lefranc, G; Lefranc, M.P.  
 Immunogenetics 30, 250-257, 1989  
 A;Reference number: A60764; MUID:90007613; PMID:2571587  
 A;Accession: A60764  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-377 <HUC>  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM3>  
 C;Keywords: immunoglobulin homology <IM3>  
 P:20-85/Domain: immunoglobulin homology <IM3>  
 Query Match Score 40.3%; Score 1143; DB 2; Length 377;  
 Best Local Similarity 64.4%; Pred. No. 1.e-69;  
 Matches 230; Conservative 17; Mismatches 56; Indels 54; Gaps 7;

Qy 194 LLIQNSLY-----TIPKOFFGSHLPPAFHLNPNLCEFLRRLQDNARENVYWK 247  
 Db 56 VLQSGGLYLSSSVVTVSSSLGT-----QTYTCN-----VNHKPSNTKVD 96

Qy 248 QVVDVKAVTNSVASY-----QCDNSDKFVKPVYKYPGK-----GCPTLGDGEGDTDLYD 294  
 Db 97 R-VELKTPGDTHTCPRPEPKSCDTPPCPRPEPKSCD----- 151

Qy 295 YPEEDTEGKVKRPHTCPRPEPKSCDTPPCPRPEPKSCD----- 354  
 Db 152 -----TTPPCPRCPAPELGGPAPVFLPPKPKDTLMISRTPEVTCVVDVSHD 200

Qy 355 PEVKFNVYTDGVVHNAKTKPREFQYNSYTRVSVLTVHQDLNGKEYKCKVSNKALP 414  
 Db 201 PEQVKWYTDGVVHNAKTKPREFQYNSYTRVSVLTVHQDLNGKEYKCKVSNKALP 260

Qy 415 PIETKISKKGOPREPOVYTLPPSREEMTKNOVSLLTCLVKGFYPSDIAVEWESNGOPENN 474  
 Db 261 PIETKISKKGOPREPOVYTLPPSREEMTKNOVSLLTCLVKGFYPSDIAVEWESNGOPENN 320

Qy 475 YKTPPPVLDSDGSFPLYSLKSLTVKSRMKGQNVFSCSYVHEALHNRTQKSLSLSPGK 531  
 Db 3221 YNTPPPVLDSDGSFPLYSLKSLTVKSRMKGQNVFSCSYVHEALHNRTQKSLSLSPGK 377

RESULT 10

G3HWWI 19 Gamma-3 heavy chain disease proteins - human  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Dec-1979 #sequence\_revision 23-Oct-1981 #text\_change 16-Jul-1999  
 C;Accession: A90442; A9219; A93915; A02149  
 R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

RESULT 9  
 G4HWWI 19 Gamma-4 chain C region - human

Biochemistry 19, 4304-4308, 1980  
 A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-  
 A;Reference number: A90442; MUID:81021548; PMID:6774747  
 A;Contents: heavy chain disease protein Wis  
 A;Molecule type: protein  
 A;Residues: 1-289 <FRM>  
 A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain  
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004  
 C;Accession: A91440; A90490; A9398; A0245; A94116; A02161.  
 R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
 Immunogenetics 18, 387-397, 1983  
 A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot  
 A;Reference number: A91749; MUID:8103030; PMID:6313520  
 A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W  
 A;Accession: A92219  
 A;Molecule type: protein  
 A;Residues: 12-97 <MC>  
 A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma  
 C:Sequence (12-28)  
 A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter  
 R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, B.E.  
 A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the  
 A;Reference number: A90198; MUID:77021516; PMID:823945  
 A;Contents: heavy chain disease protein zuc, partial sequence corresponding to residues  
 A;Accession: A90198  
 A;Molecule type: protein  
 A;Residues: 59-125, 128-225, 228-289 <WOL>  
 A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the  
 R;Alexander, A.; Steinmetz, M.; Barrault, D.; Frangione, B.; Franklin, B.C.; Hood, L.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982  
 A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion  
 A;Reference number: A93915; MUID:82247835; PMID:6608505  
 A;Contents: heavy chain disease protein Cmm  
 A;Molecule type: mRNA  
 A;Residues: 12-10; 72-114; 116-125; 'E', 127-133; 'L', 135-136; 'E', 138; 'Y', 140-154; 'D', 156-157  
 A;Note: a carboxy-terminal Lys is removed posttranslationally  
 C;Comment: The heavy chain disease protein Wis is shown.  
 C;Genetics:  
 A;Cross-references: GDB:IGHG3  
 A;Genes: GDB:IGHG3  
 A;Map: Position: 14q2.1-14q32.3 OMIM:147120  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid  
 F;203-270/Domain: immunoglobulin homology <IM>  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 Query Match 39.3% Score 1116.5; DB 1; Length 289;  
 Best Local Similarity 78.7%; Pred. No. 7.2e-68; Mismatches 11; Indels 25; Gaps 2;  
 Matches 210; Conservative 35; Gaps 30; Gaps 3;  
 Query 264 CDNSDKPKPVYKPGKCPGCPDGDGTLDIYDYPEEDTEGDKVRPHTCPPCAPEALGAPS 323  
 Db 48 CDTPPPCKPDKTLMISRTPEVTCVWVDVSHEDPEVKENWYDGVVEVHNATKPKREQYNST 383  
 Query 324 VELFPPKPKDGTLMISRTPEVTCVWVDVSHEDPEVKENWYDGVVEVHNATKPKREQYNST 383  
 Db 83 VPLFPKPKDGTLMISRTPEVTCVWVDVSHEDPEVQKWTVDGVQVHNATKPKREQYNST 142  
 Query 384 YRVPSVLTQVHODWNLNGKEYKCKVSNKALPPIEKTISKAKGQPEPQYTLPPREEMT 443  
 Db 143 FRRVPSVLTQVHQNWLQGKEYKCKVSNKALPPIEKTISKAKGQPEPQYTLPPREEMT 202  
 Query 444 KNQVSLTCLVKGRPSDIAVEMESNGOPENNYKTPPKVLDSDGSFLYSLTVDKSRWQQ 503  
 Db 203 KNQVSLTCLVKGRPSDIAVEMESNGOPENNYKTPPKVLDSDGSFLYSLTVDKSRWQQ 262  
 Query 504 GNVPSCSVMEBALNHYTKQSLSLSG 530  
 Db 161 RTARPPLREQQFNSTIRVSTLPLTQHDLRGEFKCKVHNLKALPPIEKTISKARQPL 220

Db 263 GNIFSSCSVMEBALNHYTKQSLSLSG 289  
 RESULT 11  
 GHRB  
 Ig Gamma chain C region - rabbit  
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004  
 C;Accession: A91440; A90490; A9398; A0245; A94116; A02161.  
 R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
 Immunogenetics 18, 387-397, 1983  
 A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot  
 A;Reference number: A91749; MUID:8103030; PMID:6313520  
 A;Accession: A91749  
 A;Molecule type: mRNA  
 A;Residues: 1-323 <EBR>  
 A;Cross-references: UNIPROT: P01870  
 A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr  
 R;Pratt, D.M.; Mole, L.E.  
 Biochem. J. 151, 337-349, 1975  
 A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulins  
 A;Reference number: A90290; MUID:76135469; PMID:1243651  
 A;Molecule type: protein  
 A;Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>  
 A;Accession: A90290  
 A;Molecule type: protein  
 A;Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>  
 A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain  
 R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
 A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain  
 A;Accession: A93282; MUID:83229917; PMID:6193512  
 A;Molecule type: mRNA  
 A;Residues: 88-103 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>  
 A;Accession: A93928  
 A;Cross-references: GB: M1642; NID: 916111; PID: 911289; 11; PID: G15112  
 A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker  
 R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
 Biochem. J. 116, 249-259, 1970  
 A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin  
 A;Accession: A90245; MUID:70110015; PMID:5461106  
 A;Accession: A90245  
 A;Molecule type: protein  
 A;Residues: 132-141, 'E', 145-161 <FRU>  
 R;Hill, R.L.; Leboritz, H.E.; Fellows Jr., R.E.; Delaney, R.  
 in Gamma Globulins, Nobel Symp. 3, Kilander, J., ed., pp.109-127, Almqvist and Wiksell,  
 A;Accession: A94416  
 A;Accession: A94416  
 A;Molecule type: protein  
 A;Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',  
 A;Note: this has the e15 allotypic marker, 185-Ala  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;20-82/Domain: immunoglobulin homology <IM1>  
 F;110-199/Domain: immunoglobulin homology <IM2>  
 F;226-303/Domain: immunoglobulin homology <IM3>  
 F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 32.4% Score 921; DB 1; Length 323;  
 Best Local Similarity 61.1%; Pred. No. 1.2e-54;  
 Matches 173; Conservative 35; Mismatches 45; Indels 30; Gaps 3;  
 Query 252 VKATPSNVASVQCDNSDKPKVYKPGKCPGPTLGDGTLDIYDYPEEDTEGDK-VRPHTC 310  
 Db 68 VVSTPSQPTVCAV-----HPATNTKVDTVAPSTC 100  
 Query 311 -PPCPAPEALGAPSVELFPKPKDGTLMISRTPEVTCVWVDVSHEDPEVQYKFNWYDGVYV 368  
 Db 101 SKPTPPPELGGPSVFIFFPKPKDGTLMISRTPEVTCVWVDVSDODPEVQFTWVNNNEQV 160  
 Query 369 HNAKTKPKEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPPIEKTISKAKGQPER 428  
 Db 161 RTARPPLREQQFNSTIRVSTLPLTQHDLRGEFKCKVHNLKALPPIEKTISKARQPL 220

Query 429 EPOQYTLPPSREEMTKNOVSLSLCLVKGFPSPDIANEWSNGOPENNYKTTTPVLDSPGSF 488  
 Database 221 EPRVYTMGGPREELSSRSVSLTMINGPPSPDISEWENKGKAEDNKKTPAVLDSPGSY 280

Query 489 FLYSLKTYDKSRWQOGNVEFCSYMEALHNHYTOKSLSLSPGK 531  
 Database 281 FLYNLKSVETSEWORGDVETCSYMEALHNHYTQKSISRSRPGK 323

RESULT 12  
 ID:147160  
 Ig gamma 2b chain constant region - pig (fragment)  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C;Accession: I47160  
 J. Immunol. 153, 3565-3573, 1994.  
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single IgG2b chain constant region - pig (fragment)  
 A;Reference number: 147158; MUID:95015845;  
 A;Accession: I47160  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PMID:7930579  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>  
 C;Genetics:  
 A;Gene: IgG2b  
 C;Gene: IgG2b  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>  
 F;133-202/Domain: immunoglobulin homology <IMM>  
 A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PMID:7930579  
 Query Match 32.2%; Score 913; DB 2; Length 328;  
 Best Local Similarity 71.6%; Prd. No. 4.2e-54;  
 Matches 166; Conservative 31; Mismatches 31; Indels 4; Gaps 3;

Query 302 GDKVRPHPTCPCPAPEALGAPSFLPPKPKDTLMISRPEVTCVYVDVSHEDEPEVTKFNW 361  
 Database 99 GTKTKP-PPCIPACESPS-PSVFIFFPKPKDTLMISRPEVTCVYVDVSQENPEVQFW 156

Query 362 YVDGVEVHNAYKTKPREEQYNTSYRVVSVLTQHQDWLNGKEYKCKVSNKALPVPIETIS 421  
 Database 157 YVDGVEVHNAYKTKPREEQYNTSYRVVSVLTQHQDWLNGKEYKCKVSNKALPVPIETIS 216

Query 422 KAKGQPREPQVTLPPSREEMTKNOVSLSLCLVKGFPSPDIANEWSNGQ--PENNYKTTP 479  
 Database 217 KAKGQPREPQVTLPPSREEMTKNOVSLSLCLVKGFPSPDIANEWSNGQ--PENNYKTTP 276

Query 480 PVLDSDGSFLYSLKTYDKSRWQOGNVEFCSYMEALHNHYTOKSLSLSPGK 531  
 Database 277 PVLDSDGSFLYSLKTYDKSRWQOGNVEFCSYMEALHNHYTQKSISRSRPGK 328

RESULT 13  
 ID:147159  
 Ig gamma 2a chain constant region - pig (fragment)  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C;Accession: I47159  
 J. Immunol. 153, 3565-3573, 1994.  
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single IgG2a chain constant region - pig (fragment)  
 A;Reference number: 147158; MUID:95015845;  
 A;Accession: I47159  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PMID:7930579  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>  
 C;Genetics:  
 A;Gene: IgG2a  
 C;Gene: IgG2a  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>  
 F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 32.2%; Score 913; DB 2; Length 328;  
 Best Local Similarity 71.6%; Prd. No. 4.2e-54;  
 Matches 166; Conservative 31; Mismatches 31; Indels 4; Gaps 3;

A; Cross-references: EMBL:U03778; NID:9431121; PIDN:AAA52216.1; PID:g433122  
 C; Genetics:  
 A; Gene: IgG1  
 C; Superfamily: immunoglobulin C region; immunoglobulin homology  
 F; 133-202/Domain: immunoglobulin homology <IMM>

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Query Match      31.5%;      Score 893.5;      DB 2;      Length 328;  
 Best Local Similarity 68.7%;      Pred. No. 8.6e-53;  
 Matches 167;      Conservative 29;      Mismatches 40;      Indels 7;      Gaps 3;

Qy 295 YPBEDTEGDK ---VRBHTCPCCPAPAEALGAPSVELFPKPKDTLMISRTPEVTCVVVDV 350  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 87 HPATTTKVDKRKGIIHQQTCPICPGCEVAG-PSVFLPPKPKDTLMISQTPEVTCVVVDV 145

Qy 351 SHEDPEVRFNWWYDGEVHNACTKTPREQNSTYRVRVSLLTVLHQDWLNGKEYKCKVSNK 410  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 146 SKEHAEVQFSWYDGEVHTAETRKEEQNSTYRVRVSLLPIQHQDWLKGKEFCKKVNNV 205

Qy 411 ALFPVPIRKTIKAKGOPREPOVYTLPSSREEMTKNQVSLCLVKGFYPSDTAVENESNGQ 470  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 2016 DLAPAPTRITKAKGOSREPOVYTLPSSREEMTKNQVSLCLVKGFYPSDTAVENESNGQ 265

Qy 471 --PENNYKTTTPVFLDSGGFFFLYSKLTVTDKSRWQGNVFSCSVMEHEALNNHYTOKSLSLS 528  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 266 PEPENTYRTTPQQDVTGTFFLYSKLAVIDKARWDIGDKFECAVMEHEALNNHYTOKSISKT 325

Qy 529 POK 531  
 :|  
 Db 326 QSK 328

Search completed: May 24, 2005, 06:09:00  
 Job time: 44 secs